

09/002 485

<221> polyA_signal

<222> 510..515

<221> polyA_site

<222> 530..542

<400> 68

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tggtacttag ggtcaagget tgggtcttgc cccgcaaacc cttgggacga cccggcccca    60
gcgcagct atg aac ctg gag cga gtg tcc aat gag gag aaa ttg aac ctg    110
      Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu
            -70                -65                -60
tgc cgg aag tac tac ctg ggg ggg ttt gct ttc ttg cct ttt ctc tgg    158
Cys Arg Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp
            -55                -50                -45
ttg gtc aac atc ttc tgg ttc tac cga gag gcc ttc ctt gtc cca gcc    206
Leu Val Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala
            -40                -35                -30
tac aca gaa cag agc caa atc aaa ggc tat gtc tgg cgc tca gct gtg    254
Tyr Thr Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val
            -25                -20                -15
ggc ttc ctc ttc tgg gtg ata gtg ctc acc tcc tgg atc acc atc ttc    302
Gly Phe Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe
            -10                -5                1                5
cag atc tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc    350
Gln Ile Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe
            10                15                20
acc ata ccc ctg ggc acc ccc tgacaacttc tgcacatact ggggccctgc    401
Thr Ile Pro Leu Gly Thr Pro
            25
ttattctccc aggacaggct ccttaaagca gaggagcctg tcctgggagc cccttctcaa    461
actcctaaga cttgttctca tgtccacagt tctctgtga catcccccaa taaaggaccc    521
taactttcaa aaaaaaaaaa a    542

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<210> 69

<211> 1174

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..757

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_site

<222> 1160..1174

<400> 69

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g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag    49
      Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
            -65                -60                -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc    97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
            -50                -45                -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca    145

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Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
-35 -30 -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct 193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20 -15 -10 -5
ggg gcc cag cct caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc 241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
1 5 10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat 289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
15 20 25
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta 337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
30 35 40
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag 385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45 50 55 60
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc 433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
65 70 75
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc 481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
80 85 90
atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac 529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
95 100 105
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag 577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
110 115 120
aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg 625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
125 130 135 140
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat tca gac 673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
145 150 155
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggt 721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
160 165 170
gag gcc aaa gat ggc agc aac ctc tgc ttc agc aaa tgattgtgta 767
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
175 180
accctggggc acttggtcccc ctctggacct gattcaccga tttggaagtt ttagcccta 827
gctgatactc aatggactag gcctcctcac ttgtcaatag tgtttccagg ctgggcgcag 887
tggctcatgc ctgtggtccc ggcacttcgg gaggccgagt ggggtggctc acctgaggtc 947
aggagttcga gaccatcctg gccaacatgg tgaaacccca tctccactaa aatgcaaaaa 1007
attagccagg tgtggtggcg ggcacctgta gtctcagcta ctcgaggagga tgaggcagga 1067
aaatcgcttg aaccaggag gtggaggttg cagttgagct gagatcgtgc cattgcactc 1127
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<210> 70

<211> 1285

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..1051

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix
score 7.3
seq LRLILSPLPGAQP/QQ

<221> polyA_signal
<222> 1248..1253

<221> polyA_site
<222> 1272..1285

<400> 70

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      -65                      -60                      -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc      97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50                      -45                      -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca      145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35                      -30                      -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct      193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20                      -15                      -10                      -5
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc      241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
      1                      5                      10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat      289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15                      20                      25
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta      337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30                      35                      40
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag      385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
      45                      50                      55                      60
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc      433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
      65                      70                      75
agg ctg aag atc ccc ccc ttt gag aag gcc cgc tcg gtc ctg gag gcc      481
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala
      80                      85                      90
ctg cag cag cac agg ccg agc ccg gag ctg acc ctg agc cag aag ata      529
Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile
      95                      100                      105
agg acc aag ctg cag aat cca gac ctg ctg gag cta tgt cac tca gtg      577
Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Cys His Ser Val
      110                      115                      120
ccc aag gaa gtg gac cag ttg ggg ggc agg ggc tac ggg tca gag agc      625
Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser
      125                      130                      135                      140
ggg gag gag gac ttt gct gcc ttt cga gcc tgg ctg cgc tgc tat ggc      673
Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly
      145                      150                      155
atg cca ggc atg agc tcc ctg cag gac egg cat ggc cgt acc atc tgg      721
Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp
      160                      165                      170
ttc cag ggg gat cct gga ccg ttg gca ccc aaa ggg cgc aag tcc cgc      769
Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
      175                      180                      185
aaa aag aaa tcc aag gcc aca cag ctg agt cct gag gac aga gtg gag      817
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
      190                      195                      200

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gac gct ttg cct cca agc aag gcc cct tcc aag aca cga agg gca aag      865
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
205                210                215                220
aga gac ctt cct aag agg act gca acc cag cgg cct gag ggg acc agc      913
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
                225                230                235
ctc cag cag gac cca gaa gct ccc aca gtg ccc aag aag ggg agg agg      961
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
                240                245                250
aag ggg cga cag gca gcc tct ggc cac tgc aga ccc cgg aag gtc aag      1009
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
                255                260                265
gct gac atc cca tcc ttg gaa cca gag ggg acc tca gcc tct      1051
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
                270                275                280
tagcaggagg ctctccttgc ttgcactcac cctttcttat tgtcttgccc tgcctctggg      1111
ggtctgaatt tttgggagca ggcaatatct gaaggtgcaa acaggcccta cggctgttcc      1171
ctgcacaact ctcattggtt taattgtacc ccattctcca catctttaaa gtcattgtga      1231
aaaatgctgc atttttaata aactgatata tttgaactcc aaaaaaaaaa aaaa      1285

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<210> 71

<211> 1398

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 2..1171

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_signal

<222> 1368..1373

<221> polyA_site

<222> 1386..1398

<400> 71

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                -65                -60                -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc      97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
                -50                -45                -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca      145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
                -35                -30                -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct      193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
                -20                -15                -10                -5
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc      241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                1                5                10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat      289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
                15                20                25

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gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta	337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu	
30 35 40	
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag	385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys	
45 50 55 60	
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc	433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe	
65 70 75	
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc	481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro	
80 85 90	
atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac	529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn	
95 100 105	
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag	577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu	
110 115 120	
aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg	625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro	
125 130 135 140	
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat cca gac	673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp	
145 150 155	
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggg	721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly	
160 165 170	
ggc aga ggc tac ggg tca gag agc ggg gag gag gac ttt gct gcc ttt	769
Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe	
175 180 185	
cga gcc tgg ctg cgc tgc tat ggc atg cca ggc atg agc tcc ctg cag	817
Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln	
190 195 200	
gac cgg cat ggc cgt acc atc tgg ttc cag ggg gat cct gga ccg ttg	865
Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu	
205 210 215 220	
gca ccc aaa ggg cgc aag tcc cgc aaa aag aaa tcc aag gcc aca cag	913
Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln	
225 230 235	
ctg agt cct gag gac aga gtg gag gac gct ttg cct ccg agc aag gcc	961
Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala	
240 245 250	
cct tcc agg aca cga agg gca aag aga gac ctt cct aag agg act gca	1009
Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala	
255 260 265	
acc cag cgg cct gag ggg acc agc ctc cag cag gac cca gaa gct ccc	1057
Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro	
270 275 280	
aca gtg ccc aag aag ggg agg agg aag ggg cga cag gca gcc tct ggc	1105
Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly	
285 290 295 300	
cac tgc aga ccc cgg aag gtc aag gct gac atc cca tcc ttg gaa cca	1153
His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro	
305 310 315	
gag ggg acc tca gcc tct tagcaggagg ctctccttgc ttgcactcac	1201
Glu Gly Thr Ser Ala Ser	
320	
cctttcttat tgtcttgccc tgcattctggg ggtctgaatt tttgggagca ggcaatatct	1261
gaaggtgcaa acaggcccta cggctgttcc ctgcacaact ctcatggttt taattgtacc	1321
ccatcttcca catctttaaa gctcatgtga aaaatgctgc atttttaata aactgatata	1381
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<210> 72
 <211> 821
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..611

<221> sig_peptide
 <222> 42..287
 <223> Von Heijne matrix
 score 4.4
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 787..792

<221> polyA_site
 <222> 808..821

<400> 72
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 -80
 tgt gct gtg gtc ctg gcc cag tac ctt tgg ttt cac aga aga tct ctg 104
 Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe His Arg Arg Ser Leu
 -75 -70 -65
 cca ggc aag gcc atc tta gag att gga gca gga gtg agc ctt cca gga 152
 Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly Val Ser Leu Pro Gly
 -60 -55 -50
 att ttg act gcc aaa tgt ggt gca gaa gta ata ctg tca gac agc tca 200
 Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile Leu Ser Asp Ser Ser
 -45 -40 -35 -30
 gaa ctg cct cac tgt ctg gaa gtc tgt cgg caa agc tgc caa atg aat 248
 Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln Ser Cys Gln Met Asn
 -25 -20 -15
 aac ctg cca cat ctg cag gtg gta gga cta aca tgg ggt cat ata tct 296
 Asn Leu Pro His Leu Gln Val Val Gly Leu Thr Trp Gly His Ile Ser
 -10 -5 1
 tgg gat ctt ctg gct cta cca cca caa gat att atc ctt gca tct gat 344
 Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile Ile Leu Ala Ser Asp
 5 10 15
 gtg ttc ttt gaa cca gaa gat ttt gaa gac att ttg gct aca ata tat 392
 Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile Leu Ala Thr Ile Tyr
 20 25 30 35
 ttt ttg atg cac aag aat ccc aag gtc caa ttg tgg tct act tat caa 440
 Phe Leu Met His Lys Asn Pro Lys Val Gln Leu Trp Ser Thr Tyr Gln
 40 45 50
 gtt agg agt gct gac tgg tca ctt gaa gct tta ctc tac aaa tgg gat 488
 Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu Leu Tyr Lys Trp Asp
 55 60 65
 atg aaa tgt gtc cac att cct ctt gag tct ttt gat gca gac aaa gaa 536
 Met Lys Cys Val His Ile Pro Leu Glu Ser Phe Asp Ala Asp Lys Glu
 70 75 80
 gat ata gca gaa tct acc ctt cca gga aga cat aca gtt gaa atg ctg 584
 Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His Thr Val Glu Met Leu
 85 90 95
 gtc att tcc ttt gca aag gac agt ctc tgaattatac ctacaacctg 631
 Val Ile Ser Phe Ala Lys Asp Ser Leu

100	105	
ttctgggaca gtatcaatac tgatgagcaa cctggcacac aaactatgag cagaccactt		691
cagcttgaga atgcagtggg tctgaagatg gtcaagtctg tctgccttag attttgatgt		751
cacctagaca acacttaaac tcatatgaaa caaaaattaa aatacgattt acaagtaaaa		811
aaaaaaaaaa		821

<210> 73
 <211> 916
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 62..916

<221> sig_peptide
 <222> 62..757
 <223> Von Heijne matrix
 score 4.2
 seq LVTPAALRPLVLG/GN

<221> polyA_site
 <222> 904..916

<400> 73	
cctgaatgac ttgaatgttt ccccgctga gctaacagtc catgtgggtg attcagctct	60
g atg gga tgt gtt ttc cag agc aca gaa gac aaa cgt ata ttc aag ata	109
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile	
-230 -225 -220	
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta	157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu	
-215 -210 -205	
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc	205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg	
-200 -195 -190 -185	
gta cac ttg atg ggg gac aac tta tgc aat gat ggc tct ctc ctg ctc	253
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu	
-180 -175 -170	
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc	301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg	
-165 -160 -155	
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg	349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val	
-150 -145 -140	
ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att	397
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile	
-135 -130 -125	
cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag	445
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys	
-120 -115 -110 -105	
gta gaa tgg ata ttt tca gga cgg cgc gca aag gag gag att gta ttt	493
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe	
-100 -95 -90	
cgt tac tac cac aaa ctc agg atg tct gcg gag tac tcc cag agc tgg	541
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp	
-85 -80 -75	
ggc cac ttc cag aat cgt gtg aac ctg gtg ggg gac att ttc cgc aat	589
Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn	
-70 -65 -60	
gac ggt tcc atc atg ctt caa gga gtg agg gag tca gat gga gga aac	637

Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys	
115 120 125	
gta gaa tgg ata ttt tca gga cgg cgc gca aag gta aca agg agg aaa	493
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys	
130 135 140	
cat cac tgt gtt aga gaa ggc tct ggc tgatgggtatc aggacaaaagg	540
His His Cys Val Arg Glu Gly Ser Gly	
145 150	
tagaatcagg cacatgagga ggtgttgcaa gagcctgggc tttggtgctt atcagaactg	600
gaccttctcc tagcaatttc agctttcttg tgggaaagg aactccaatg aagaacaaga	660
acaagaagat gatgatgatg cttaactttt tggatgccga tatgagattg tacatgtaaa	720
gcattttgta taagacttgg cccctgcatt ttagtttctt tctttctccc ttttcttctg	780
tatagagtcc atgggagaat gagggagatg atttttgttg cccagccaag aaagcaatgg	840
gctagacatt aaaatgatta cacttttatt cttactgggg ttagttctgt gagttttcat	900
ctgtgcccc ttgccccatt tatgtgatgg agggaaattt catgggtact tcacgtgttg	960
ggattgattg atcctggggg ccagggtgaa gggatattt cgggacctct ataaagcagg	1020
aagaagcaag tttattcttt agaccagtag ctctcaacca tgatgtggtc atatatattat	1080
gggtcaacat gtgttgtggg gatatcccaa gtaacttggt attaataaaa gttaagttgc	1140
aaaaaaaaaa aaa	1153

<210> 75

<211> 1517

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..167

<400> 75

ctctgaaatg cttgtctttt atg ctg gna ggt gac cat agg gct ctg ctt tta	53
Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu	
1 5 10	
aag ata tgg ctg ctt caa agg cca gag tca cag gaa gga ctt ctt cca	101
Lys Ile Trp Leu Leu Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro	
15 20 25	
ggg aga tta gtg gtg atg gag agg aga gtt aaa atg acc tca tgt cct	149
Gly Arg Leu Val Val Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro	
30 35 40	
tct tgt cca cgg ttt tgt tgatgtttca ctcttctaata gcaagggtct	197
Ser Cys Pro Arg Phe Cys	
45	
cacactgtga accacttagg atgtgatcac tttcagggtg ccaggaatgt tgaatgtctt	257
tggtcagtt catttaaaaa agatatctat ttgaaagtct tcagagttgt acatatgttt	317
cacagtacag gatctgtaca taaaagtctt tttcctaacc cattcaccaa gagccaatat	377
ctaggcattt tcttggttagc acaaattttt ttattgctta gaaaattgtc ctcttgttta	437
tttctgtttg taagacttaa gtgagttagg tctttaagga aagcaacgct cctctgaaat	497
gcttgtcttt tatgctggga ggtgaccata gggctctgct tctaaagata tggctgcttc	557
aaaggccaga gtcacaggaa ggacttcttc caggagatt agtggtgatg gagaggagag	617
ttaaaatgac ctcatgtcct tcttgccac ggttttgttg agttttcact cttctaattgc	677
aagggtctca cactgtgaac cacttaggat gtgatcactt tcagggtggcc aggaatgttg	737
aatgtctttg gtcagttca ttttaaaaaag atatctattt gaaagttctc agagttgtac	797
atatgtttca cagtacagga tctgtacata aaagtttctt tctaaacca ttcaccaaga	857
gccaatatct aggcattttc ttggtagcac aaattttctt attgcttaga aaattgtcct	917
ccttgttatt tctgtttgta agacttaagt gagttaggct ttaaggaaa gcaacgctcc	977
tctgaaatgc ttgtcttttna tgctgggagg tgaccatagg gctctgcttt taaagatag	1037
gctgtcttcaa aggccagagt cacaggaagg acttcttcca gggagattag tgggtgatgga	1097
gaggagagtt aaaaatgacct catgtccttc ttgtccacgg tttgttgag ttttactct	1157
tctaatagcaa gggcttcaca ctgtgaacca cttaggatgt gatcactttc aggtggccag	1217
gaatgttgaa tgtctttggc tcagttcatt taaaaaagat atctatttga aagttctcag	1277

```

agttgtacat atgtttcaca gtacaggatc tgtacataaa agttttcttc ctaaaccatt 1337
caccaagagc caatatctag gcattttctt ggtagcacia attttcttat tgcttagaaa 1397
attgtcctcc ttgttatttc tgtttgtaag acttaagtga gttagggtctt taaggaaagc 1457
aacgctcctc tgaaatgctt gtcttttatg ctgggagggtg accatagggc tctgctttta 1517

```

```

<210> 76
<211> 526
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 22..318

```

```

<221> sig_peptide
<222> 22..93
<223> Von Heijne matrix
      score 4.6
      seq FFIFCSLNTLLLG/GV

```

```

<221> polyA_signal
<222> 497..502

```

```

<221> polyA_site
<222> 516..526

```

```

<400> 76
ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga ttt ctt cta 51
                        Met Lys Ser Ala Lys Leu Gly Phe Leu Leu
                        -20 -15
aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg ggt ggt gtt 99
Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu Gly Gly Val
                        -10 -5 1
aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat ccc tgc aaa 147
Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys
                        5 10 15
ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga tat ttc 195
Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg Tyr Phe
                        20 25 30
tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc ggc tgt 243
Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser Gly Cys
                        35 40 45 50
aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt gaa gta gcc 291
Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg Glu Val Ala
                        55 60 65
tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg tgaactcatg 338
Cys Val Ala Lys Tyr Lys Pro Pro Arg
                        70 75
aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcagactg attttgaaat 398
ctttgtaata tttccataat gctttaagct tccatatgtt tgctattttc ctgaccctag 458
ttttgtcttt cctggaaatt aactgtatga tcattagaat gaaagagtct ttctgtcaaa 518
aaaaaaaaa 526

```

```

<210> 77
<211> 352
<212> DNA
<213> Homo sapiens

```

<220>
 <221> CDS
 <222> 8..292

<221> sig_peptide
 <222> 8..118
 <223> Von Heijne matrix
 score 5.6
 seq WLLLDALLRLGDT/KK

<221> polyA_signal
 <222> 317..322

<221> polyA_site
 <222> 339..352

<400> 77
 ctgagat atg gca agt ccc gct gta aac agg tgg aaa agg cca agg ttg 49
 Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu
 -35 -30 -25
 aag ccg gtg tgg cca cgg cgc ttg gaa tcc tgg ttg ttg ctg gat gct 97
 Lys Pro Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala
 -20 -15 -10
 ctt ttg cga tta gga gat acc aaa aaa aag cga cag cct gaa gca gcc 145
 Leu Leu Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala
 -5 1 5
 aca aaa tcc tgt gtt aga agc agc tgt ggg ggt ccc agt gga gat ggg 193
 Thr Lys Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly
 10 15 20 25
 cct ccc cca tgc ctc cag cag cct gac cct cgt gcc ctg tct cag gcg 241
 Pro Pro Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala
 30 35 40
 ttc tct aga tcc ttt cct ctg ttt ccc tct ctc gct ggc aaa agt atg 289
 Phe Ser Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met
 45 50 55
 atc taattgaaac aagactgaag gatcaataaa cagccatctg ccccttcaaa 342
 Ile
 aaaaaaaaaa 352

<210> 78
 <211> 542
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..378

<221> sig_peptide
 <222> 16..84
 <223> Von Heijne matrix
 score 9.8
 seq FLLFFFLFLLTRG/SL

<221> polyA_signal
 <222> 502..507

<221> polyA_site
 <222> 522..542

<400> 78

```

cacgacctgt gggcc atg atg cta ccc caa tgg ctg ctg ctg ctg ttc ctt      51
          Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu
                    -20                    -15
ctc ttc ttc ttt ctc ttc ctc ctc acc agg ggc tca ctt tct cca aca      99
Leu Phe Phe Phe Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr
      -10      -5      1      5
aaa tat aac ctt ttg gag ctc aag gag tct tgc atc cgg aac cag gac      147
Lys Tyr Asn Leu Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp
          10          15          20
tgc gag act ggc tgc tgc caa cgt gct cca gac aat tgc gag tcg cac      195
Cys Glu Thr Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
          25          30          35
tgc gcg gag aag ggg tcc gag ggc agt ctg tgt caa acg cag gtg ttc      243
Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe
          40          45          50
ttt ggc caa tat aga gcg tgt ccc tgc ctg cgg aac ctg act tgt ata      291
Phe Gly Gln Tyr Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile
      55      60      65
tat tca aag aat gag aaa tgg ctt agc atc gcc tat ggc cgt tgt cag      339
Tyr Ser Lys Asn Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln
      70      75      80      85
aaa att gga agg cag aag ttg gct aag aaa atg ttc ttc tagtgctccc      388
Lys Ile Gly Arg Gln Lys Leu Ala Lys Lys Met Phe Phe
          90          95
tccttcttgc tgctctctcc tcctccacct gctctcctcc ctaccagag ctctgtgttc      448
accctgttcc ccagagcctc caccatgagt ggagggaagt ggggagtgat tgaaataaag      508
agctttttca atgaaaaaaaa aaaaaaaaaa aaaa      542

```

<210> 79

<211> 233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..233

<400> 79

```

gcaaaaccaa aaccagcacc gatcccgaca tagatcagtg acgtcttttt cttcag atg      59
                                     Met
                                     1
atc cta tgt ttc ctt ctt cct cat cat cgt ctt cag gaa gcc aga cag      107
Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg Gln
          5          10          15
att caa gta ttg aag atg ctg cca agg gaa aaa tta aga aga aga gaa      155
Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg Glu
      20      25      30
gag aga aaa caa ata aat ggg aaa aaa gaa agg aca aaa tat gaa aca      203
Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu Thr
      35      40      45
cca aga aaa aga gaa gga aaa aaa aaa aaa      233
Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
      50          55

```

<210> 80

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 83..340

<221> sig_peptide

<222> 83..124

<223> Von Heijne matrix

score 7.5

seq VALNLIILVPCCAA/WC

<221> polyA_signal

<222> 573..578

<221> polyA_site

<222> 607..660

<400> 80

```

gaatttgtaa aacttctgct cgtttacct gcacattgaa tacaggtaac taattggaag      60
gagaggggag atcactcttt tg atg gtg gcc ctg aac ctc att ctg gtt ccc      112
                               Met Val Ala Leu Asn Leu Ile Leu Val Pro
                               -10                               -5
tgc tgc gct gct tgg tgt gac cca cgg agg atc cac tcc cag gat gac      160
Cys Cys Ala Ala Trp Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp
                               1                               5                               10
gtg ccc cgt agc tct gct gct gat act ggg tct gcg atg cag cgg cgt      208
Val Pro Arg Ser Ser Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg
                               15                               20                               25
gag gcc tgg gct ggt tgg aga agg tca caa ccc ttc tct gtt ggt ctg      256
Glu Ala Trp Ala Gly Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu
                               30                               35                               40
cct tct gct gaa aga ctc gag aac caa cca ggg aag ctg tcc tgg agg      304
Pro Ser Ala Glu Arg Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg
                               45                               50                               55                               60
tcc ctg gtc gga gag gga tat aga atc tgt gac ctc tgacaactgt      350
Ser Leu Val Gly Glu Gly Tyr Arg Ile Cys Asp Leu
                               65                               70
gaagccaccc tgggctacag aaaccacagt cttcccagca attattacaa ttcttgaatt      410
ccttggggat tttttactgc ctttcaaag cacttaagtg ttagatctaa cgtgttccag      470
tgtctgtctg aggtgactta aaaaatcaga acaaaacttc tattatccag agtcatggga      530
gagtacaccc tttccaggaa taatgttttg ggaaacactg aaatgaaatc ttcccagtat      590
tataaattgt gtatttaaaa aaagaaactt ttctgaatgc ctacctggcg gtgtatacca      650
ggcagtgtgc                                     660

```

<210> 81

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 47..541

<221> sig_peptide

<222> 47..220

<223> Von Heijne matrix

score 5.4

seq QLLDSVLWLALG/LT

<221> polyA_site

<222> 597..605

<400> 81

```

aaagtgggag gagcactagg tcttcccgctc acctccacct ctctcc atg acc cgg      55
                                     Met Thr Arg
ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg atc cca gtt cct      103
Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile Pro Val Pro
-55                               -50                               -45                               -40
cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt cca gtg cgt cca      151
Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro Val Arg Pro
                               -35                               -30                               -25
cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc ctg gac agt gtc      199
Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu Asp Ser Val
                               -20                               -15                               -10
cta tgg ctg ggg gca cta gga ctg aca atc cag gca gtc ttt tcc acc      247
Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val Phe Ser Thr
                               -5                               1                               5
act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc ctc acc ttt gac      295
Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe Leu Thr Phe Asp
10                               15                               20                               25
ctg ctc cat agg ccc gca ggt cac act ctg cca cag cgc aaa ctt ctc      343
Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg Lys Leu Leu
                               30                               35                               40
acc agg ggc cag agt cag ggg gcc ggt gaa ggt cct gga cag cag gag      391
Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly Gln Gln Glu
                               45                               50                               55
gct cta ctc ctg caa atg ggt aca gtc tca gga caa ctt agc ctc cag      439
Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu Ser Leu Gln
                               60                               65                               70
gac gca ctg ctg ctg ctg ctc atg ggg ctg ggc ccg ctc ctg aga gcc      487
Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu Leu Arg Ala
                               75                               80                               85
tgt ggc atg ccc ttg acc ctg ctt ggc ctg gct ttc tgc ctc cat cct      535
Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys Leu His Pro
90                               95                               100                               105
tgg gcc tgagagcccc tccccacaac tcagtgtcct tcaaatatac aatgaccacc      591
Trp Ala
cttcttcaaa aaaa      605

```

<210> 82

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..285

<221> sig_peptide

<222> 46..150

<223> Von Heijne matrix

score 3.6

seq LEPLSSSAACNG/KE

<221> polyA_signal

<222> 364..369

<221> polyA_site

<222> 385..396

<400> 82

```

cctctacagg aatcagactc agcctctttt ggttttcagt gaagt atg cct ttt caa      57
                               Met Pro Phe Gln
                               -35
ttt gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca      105
Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser
-30                -25                -20
att gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag      153
Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys
-15                -10                -5                1
gag atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc      201
Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys
                    5                10                15
ctg aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag      249
Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys
                20                25                30
cca cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt      295
Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
                35                40                45
aagtccttttg tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctgggtgatct      355
ggtaaacaaa taaaagtggg ggcaccttca aaaaaaaaaa a      396

```

<210> 83

<211> 432

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..240

<221> sig_peptide

<222> 22..84

<223> Von Heijne matrix

score 12

seq VLVLCVLLLQAQG/GY

<221> polyA_signal

<222> 397..402

<221> polyA_site

<222> 421..432

<400> 83

```

gctcacgctc tggtcagagt t atg gca ccc cag act ctg ctg cct gtc ctg      51
                               Met Ala Pro Gln Thr Leu Leu Pro Val Leu
                               -20                -15
gtt ctc tgt gtg ctg ctg ctg cag gcc cag gga gga tac cgt gac aag      99
Val Leu Cys Val Leu Leu Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys
-10                -5                1                5
atg agg atg cag aga atc aag gtc tgt gag aag cga ccc agc ata gat      147
Met Arg Met Gln Arg Ile Lys Val Cys Glu Lys Arg Pro Ser Ile Asp
                    10                15                20
cta tgc atc cac cac tgt tca tgt ttc caa aag tgt gaa aca aat aag      195
Leu Cys Ile His His Cys Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys
                    25                30                35
ata tgc tgt tca gcc ttc tgt ggg aac att tgt atg agc atc cta      240
Ile Cys Cys Ser Ala Phe Cys Gly Asn Ile Cys Met Ser Ile Leu
                40                45                50

```

```

tgagtgggag agtgggctgg gatgtgcac ctgctccctg aacccttcca tccgagactg 300
tgcccacatc cgaagcacia ggacatcaaa tcatcagcac aagaacatca acaggaatgc 360
caccctcccc agtgtctgaa ctccctgtcc ctgtcaaatg aaccagaaca aatgccccatg 420
aaaaaaaaaa aa 432

```

<210> 84
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..382

<221> polyA_site
 <222> 408..420

```

<400> 84
gcttgctga ccccatgtc gcctctgtag gtagaagaag tatgtcttcc tggacccct 60
ggctggtgct gtaacaaaga cccatgtg atg ctg ggg gca gag aca gag gag 112
                               Met Leu Gly Ala Glu Thr Glu Glu
                               1           5
aag ctg ttt gat gcc ccc ttg tcc atc agc aag aga gag cag ctg gaa 160
Lys Leu Phe Asp Ala Pro Leu Ser Ile Ser Lys Arg Glu Gln Leu Glu
   10           15           20
cag cag gtc cca gag aac tac ttc tat gtg cca gac ctg ggc cag gtg 208
Gln Gln Val Pro Glu Asn Tyr Phe Tyr Val Pro Asp Leu Gly Gln Val
   25           30           35           40
cct gag att gat gtt cca tcc tac ctg cct gac ctg ccc ggc att gcc 256
Pro Glu Ile Asp Val Pro Ser Tyr Leu Pro Asp Leu Pro Gly Ile Ala
           45           50           55
aac gac ctc atg tac att gcc gac ctg ggc ccc ggc att gcc ccc tct 304
Asn Asp Leu Met Tyr Ile Ala Asp Leu Gly Pro Gly Ile Ala Pro Ser
           60           65           70
gcc cct ggc acc att cca gaa ctg ccc acc ttc cac act gag gta gcc 352
Ala Pro Gly Thr Ile Pro Glu Leu Pro Thr Phe His Thr Glu Val Ala
           75           80           85
gag cct ctc aag acc tac aag atg ggg tac taacagcacc accaccgccc 402
Glu Pro Leu Lys Thr Tyr Lys Met Gly Tyr
           90           95
ccaccaaaaa aaaaaaaaaa 420

```

<210> 85
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..415

<221> sig_peptide
 <222> 80..142
 <223> Von Heijne matrix
 score 5.4
 seq TFCLIFGLGAVWG/LG

<221> polyA_signal

<222> 471..476

<221> polyA_site

<222> 488..501

<400> 85

```

ccccgttgat tccaagaacc tcttcgatat ttatttttat ttttaaagag ggagacgatg      60
gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt      112
                Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys
                -20                -15
ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc      160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser
-10                -5                1                5
cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc      208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr
                10                15                20
gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc      256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu
                25                30                35
ttt caa gat act ccc aga agc ata aaa gca tcc act gct aca gct gaa      304
Phe Gln Asp Thr Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu
                40                45                50
cag ttt ttt cag aag ctg aga aat aaa cat gaa ttt act att ttg gtg      352
Gln Phe Phe Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val
55                60                65                70
acc cta aaa cag acc cac tta aat tca gga gtt att ctc tca att cac      400
Thr Leu Lys Gln Thr His Leu Asn Ser Gly Val Ile Leu Ser Ile His
                75                80                85
cac ttg gat cac agg taaatgtggt tgctggagtt tcctgtgttt tcattatatg      455
His Leu Asp His Arg
                90
tgggttaaag aatatattaa agagaagtaa acaaaaaaaaa aaaaaa      501

```

<210> 86

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 152..361

<221> sig_peptide

<222> 152..283

<223> Von Heijne matrix

score 4.7

seq FLLSLSLITYCFW/DP

<400> 86

```

gacatttttac ttttttctgt taacgcttac cctagaaatt agaaatgaca ccacgtattc      60
ttagcggaagt ccagttttca gcattttgtc cttattggac aatagcaagg atattagaac      120
gtgttggttc cgcgtgcttc cgtcttgagt t atg tgc tgc tat tgt cgg ata      172
                Met Cys Cys Tyr Cys Arg Ile
                -40
ttt tgt ctt aga tgt acg tac ttt cct gtt cat tgt ggt atg tgt aat      220
Phe Cys Leu Arg Cys Thr Tyr Phe Pro Val His Cys Gly Met Cys Asn
-35                -30                -25
ttg cgt tac ttt gaa ttt tcc acg ttt tta ctt tct ttg tct ctc atc      268
Leu Arg Tyr Phe Glu Phe Ser Thr Phe Leu Leu Ser Leu Ser Leu Ile
-20                -15                -10

```

```

act tac tgc ttt tgg gac ccc ccc cat cgg ggt tca cat tcc ctc tcc      316
Thr Tyr Cys Phe Trp Asp Pro Pro His Arg Gly Ser His Ser Leu Ser
-5          1          5          10
cta gag cac act ccc ttg gat ttc ctc gag tgg ggt ctg ctg cgg      361
Leu Glu His Thr Pro Leu Asp Phe Leu Glu Trp Gly Leu Leu Arg
          15          20          25
tgaagctttc ccattttatg tgcagattat ttccagaggg tatatagaat tcaggcagct      421
gtttcgttgt agcacattaa aaatattttc ccc      454

```

<210> 87
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..307

<221> sig_peptide
 <222> 32..70
 <223> Von Heijne matrix
 score 4.2
 seq MLFSLSLLSNLNQ/IG

<221> polyA_signal
 <222> 1240..1245

<221> polyA_site
 <222> 1261..1272

```

<400> 87
gtcaggttgc accgcccttt ggttcccgag c atg ctg ttt tct ctc agc ctt      52
                               Met Leu Phe Ser Leu Ser Leu
                               -10
ctc tcc aac ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac      100
Leu Ser Asn Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His
-5          1          5          10
att cct ggc caa tca gct cag ctg ttt att tac caa atg tct tca caa      148
Ile Pro Gly Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln
          15          20          25
caa cta cag cag cag cct tcg gct aac aaa aaa gca gga aaa atc cac      196
Gln Leu Gln Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile His
          30          35          40
aac acc ccc ttc gcc aac caa cta aat cca acg caa cat ctg gca aaa      244
Asn Thr Pro Phe Ala Asn Gln Leu Asn Pro Thr Gln His Leu Ala Lys
          45          50          55
cct ttt cag caa att ctt cct ggc cgt cag tcc ggc agc ctc acc tca      292
Pro Phe Gln Gln Ile Leu Pro Gly Arg Gln Ser Gly Ser Leu Thr Ser
          60          65          70
cca ttt cta gct tgc tgaaccctaa aactaatctc caagaaggag aagcttctct      347
Pro Phe Leu Ala Cys
75
cgcagccgga gcaggtccct ttctagagat aggagaagag agagatcgct gtctcgggag      407
agaaatcaca agccgtcccg atccttctct aggtctcgta gtcgatttag gtcaaataaa      467
aggaaataga agacagtttg caagagaagt ggtgtacagg aaattacttc atttgacagg      527
agtatgtaca gaaaattcaa gttttgtttg agacttcata agcttggtgc atttttaaga      587
tggttttagct gttcaaatct gtttgtctct tgaacagtg acacaaaagt gtaattctct      647
atggtttgaa atggatcata cgaggcatgt aataccaaga attgttactt tacaatgttc      707
ccttaagcaa aattgaattt gctttgaact tttagttatg cacagactga taataaacct      767
ctaaacctgc ccagcggaag tgtgtttttt tttaaattta aatacagaaa caactggcaa      827

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aaattgaact aagatttact tttttttcca tagctgggat ataggctgca gctatagttg 887
aacaagcagt ctttaaaaac tgctgtgaaa cacaggccat cagggaaaac gaaatgctgc 947
actattaaat tagaggtttt tgaaaaatcc aactctcatc ctgggcagag gttgcctagt 1007
tggtatagaa tgtaaagttt caagaaagtt tacctttgct ttaggtcgta agttccttat 1067
ttgattgccg tatatggata catggctggt cgtgacattc tttatgtgca aatttgtgat 1127
ttcaaaaatg tcctgccagt ttaagggtac attgtagagc cgaactttga gttactgtgc 1187
aagatttttt ttcattgctgt catttgaat atgttttgtg agaatccttg ggattaaagt 1247
tttggttaca gattaaaaaa aaaaa 1272

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<210> 88

<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 114..734

<221> sig_peptide

<222> 114..239

<223> Von Heijne matrix

score 5.2

seq LLFDLVCHEFCQS/DD

<221> polyA_signal

<222> 768..773

<221> polyA_site

<222> 793..804

<400> 88

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agctgccaaa caagtacggt agttctgaaa atccagaatg gcttgatggt tac atg 116
                                         Met
cac att tta caa ctg ctt act aca gtg gat gat gga att caa gca att 164
His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile
-40 -35 -30
gta cat tgt cct gac act gga aaa gac att tgg aat tta ctt ttt gac 212
Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp
-25 -20 -15 -10
ctg gtc tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt 260
Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu
-5 1 5
caa gaa cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc 308
Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala
10 15 20
atc tat gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta 356
Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val
25 30 35
gat ctt cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa 404
Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu
40 45 50 55
cag tgt cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa 452
Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu
60 65 70
act aaa agg act gat tta acc caa gat gat ctc cac ttg aaa atc tta 500
Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile Leu
75 80 85
aag gat att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca 548
Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr

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      90      95      100
aag gag acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag 596
Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln
      105      110      115
aag tgt tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg 644
Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val
      120      125      130      135
gtg gaa gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct 692
Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala
      140      145      150
gat gac ttg gaa aaa aac ttc cca agt ttg aag gtt cag act 734
Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
      155      160      165
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa 794
aaaaaaaaaa 804

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<210> 89
 <211> 802
 <212> DNA
 <213> Homo sapiens

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 <222> 199..801

<221> polyA_signal
 <222> 780..785

<221> polyA_site
 <222> 791..802

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tgctgcaaga tctgttatcc gctctgtggt tttgtcatcc ttgctgcctg tgttgtggcc 180
tgtgttggtc tgggtgtgg atg cag gtt gct ctc aag gag gat ctg gat gcc 231
      Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala
      1      5      10
ctc aag gaa aaa ttt cga aca atg gaa tct aat cag aaa agc tca ttc 279
Leu Lys Glu Lys Phe Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe
      15      20      25
caa gaa atc ccc aaa ctt aat gaa gaa cta ctc agc aag caa aaa caa 327
Gln Glu Ile Pro Lys Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln
      30      35      40
ctt gag aag att gaa tct gga gag atg ggt ttg aac aaa gtc tgg ata 375
Leu Glu Lys Ile Glu Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile
      45      50      55
aac atc aca gaa atg aat aag cag att tct ctg ttg act tct gca gtg 423
Asn Ile Thr Glu Met Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val
      60      65      70      75
aac cac ctc aaa gcc aat gtt aag tca gct gca gac ttg att agc ctg 471
Asn His Leu Lys Ala Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu
      80      85      90
cct acc act gta gag gga ctt cag aag agt gta gct tcc att ggc aat 519
Pro Thr Thr Val Glu Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn
      95      100      105
act tta aac agc gtc cat ctt gct gtg gaa gca cta cag aaa act gtg 567
Thr Leu Asn Ser Val His Leu Ala Val Glu Ala Leu Gln Lys Thr Val
      110      115      120
gat gaa cac aag aaa acg atg gaa tta ctg cag agt gat atg aat cag 615

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Asp Glu His Lys Lys Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln
   125                130                135
cac ttc ttg aag gag act cct gga agc aac cag atc att ccg tca cct      663
His Phe Leu Lys Glu Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro
   140                145                150                155
tca gcc aca tca gaa ctt gac aat aaa acc cac agt gag aat ttg aaa      711
Ser Ala Thr Ser Glu Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys
               160                165                170
cag atg ggt gat aga tct gcc act ctg aaa aga cag tct ttg gac caa      759
Gln Met Gly Asp Arg Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln
               175                180                185
gtc acc aac aga aca gat aca gta aaa atc caa aaa aaa a a      802
Val Thr Asn Arg Thr Asp Thr Val Lys Ile Gln Lys Lys Lys
   190                195                200

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<210> 90

<211> 1490

<212> DNA

<213> Homo sapiens

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<222> 38..1174

<221> sig_peptide

<222> 38..148

<223> Von Heijne matrix

score 7.3

seq LLSACLVTWGLG/EP

<221> polyA_signal

<222> 1452..1457

<221> polyA_site

<222> 1478..1490

<400> 90

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                               Met Pro His Ser Ser Leu
                               -35
cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc cag aag gca gcc      103
His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys Ala Ala
   -30                -25                -20
ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg ggg cta gga gag      151
Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu Gly Glu
   -15                -10                -5                1
cca cca gag cac act ctc cgg tac ctg gtc ctc cac cta gcc tcc ctg      199
Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala Ser Leu
               5                10                15
cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg gct gag gag ctg      247
Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu Glu Leu
               20                25                30
cgc cac atc cac tcc agg tac cgg ggc agc tac tgg agg act gtg cgg      295
Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr Val Arg
               35                40                45
gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg ttg ctg ctg tcc      343
Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu Leu Ser
   50                55                60                65
atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc ccg ccc ttc act      391
Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly Pro Pro Phe Thr

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70								75				80				
tgg	atg	ctt	gcc	ctc	ctg	ggc	ctc	tgc	cag	gca	ctg	aac	atc	ctc	ctg	439
Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln	Ala	Leu	Asn	Ile	Leu	Leu	
			85					90					95			
ggc	ctc	aag	ggc	ctg	gcc	cca	gct	gag	atc	tct	gca	gtg	tgt	gaa	aaa	487
Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile	Ser	Ala	Val	Cys	Glu	Lys	
		100					105					110				
ggg	aat	ttc	aac	gtg	gcc	cat	ggg	ctg	gca	tgg	tca	tat	tac	atc	gga	535
Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala	Trp	Ser	Tyr	Tyr	Ile	Gly	
	115					120					125					
tat	ctg	cgg	ctg	atc	ctg	cca	gag	ctc	cag	gcc	cgg	att	cga	act	tac	583
Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln	Ala	Arg	Ile	Arg	Thr	Tyr	
130					135					140					145	
aat	cag	cat	tac	aac	aac	ctg	cta	cgg	ggt	gca	gtg	agc	cag	cgg	ctg	631
Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly	Ala	Val	Ser	Gln	Arg	Leu	
				150				155					160			
tat	att	ctc	ctc	cca	ttg	gac	tgt	ggg	gtg	cct	gat	aac	ctg	agt	atg	679
Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val	Pro	Asp	Asn	Leu	Ser	Met	
		165						170				175				
gct	gac	ccc	aac	att	cgc	ttc	ctg	gat	aaa	ctg	ccc	cag	cag	acc	ggt	727
Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys	Leu	Pro	Gln	Gln	Thr	Gly	
		180					185				190					
gac	cgt	gct	ggc	atc	aag	gat	cgg	gtt	tac	agc	aac	agc	atc	tat	gag	775
Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr	Ser	Asn	Ser	Ile	Tyr	Glu	
	195				200					205						
ctt	ctg	gag	aac	ggg	cag	cgg	gcg	ggc	acc	tgt	gtc	ctg	gag	tac	gcc	823
Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr	Cys	Val	Leu	Glu	Tyr	Ala	
210					215					220				225		
acc	ccc	ttg	cag	act	ttg	ttt	gcc	atg	tca	caa	tac	agt	caa	gct	ggc	871
Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser	Gln	Tyr	Ser	Gln	Ala	Gly	
				230					235				240			
ttt	agc	cgg	gag	gat	agg	ctt	gag	cag	gcc	aaa	ctc	ttc	tgc	cgg	aca	919
Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala	Lys	Leu	Phe	Cys	Arg	Thr	
		245						250				255				
ctt	gag	gac	atc	ctg	gca	gat	gcc	cct	gag	tct	cag	aac	aac	tgc	cgc	967
Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu	Ser	Gln	Asn	Asn	Cys	Arg	
		260				265						270				
ctc	att	gcc	tac	cag	gaa	cct	gca	gat	gac	agc	agc	ttc	tgc	ctg	tcc	1015
Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp	Ser	Ser	Phe	Ser	Leu	Ser	
		275				280					285					
cag	gag	gtt	ctc	cgg	cac	ctg	cgg	cag	gag	gaa	aag	gaa	gag	gtt	acc	1063
Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu	Glu	Lys	Glu	Glu	Val	Thr	
290					295					300					305	
gtg	ggc	agc	ttg	aag	acc	tca	gcg	gtg	ccc	agt	acc	tcc	acg	atg	tcc	1111
Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro	Ser	Thr	Ser	Thr	Met	Ser	
			310						315				320			
caa	gag	cct	gag	ctc	ctc	ctc	agt	gga	atg	gga	aag	ccc	ctc	cct	ctc	1159
Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met	Gly	Lys	Pro	Leu	Pro	Leu	
			325					330				335				
cgc	acg	gat	ttc	tct	tgag	acccag	ggtc	caccag	ccag	agcctc	cagt	gggtc	ctc			1214
Arg	Thr	Asp	Phe	Ser												
		340														
caagc	ctctg	gact	gggggc	tctcttc	cagt	ggct	gaatgt	ccagc	agagc	tatttc	cttc					1274
cacag	ggggc	cttg	caggg	aggg	tccag	acttg	acate	ttaag	atgcg	tcttg	tcccc					1334
ttggg	cagc	catttc	cccc	ctctg	agcct	cgg	gtgtctc	aacct	gtgaa	atggg	atcat					1394
aatc	actg	ctt	acctcc	cac	ggtgtt	gtgag	gactg	agtgt	gtgga	agtttt	ttcat					1454
aaact	tttga	tqcta	gtqta	ctt	aaaaaaaa											1490

<210> 91
<211> 361

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<213> Homo sapiens

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<222> 26..361

<221> polyA_site
<222> 350..361

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1 5
acc ttg aag gcc cta cgc agt tcc gac aaa ggt cgc ctt tgc tac tac 100
Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr Tyr
10 15 20 25
cgc gac tgg ctg ctg cgg cgc gag gat gtt tta gaa gaa tgt atg tct 148
Arg Asp Trp Leu Leu Arg Arg Glu Asp Val Leu Glu Glu Cys Met Ser
30 35 40
ctt ccc aag cta tct tct tat tct gga tgg gtg gta gag cac gtc cta 196
Leu Pro Lys Leu Ser Ser Tyr Ser Gly Trp Val Val Glu His Val Leu
45 50 55
ccc cat atg cag gag aac caa cct ctg tct gag act tcg cca tcc tct 244
Pro His Met Gln Glu Asn Gln Pro Leu Ser Glu Thr Ser Pro Ser Ser
60 65 70
acg tca gct tca gcc cta gat caa ccc tca ttt gtt ccc aaa tct cct 292
Thr Ser Ala Ser Ala Leu Asp Gln Pro Ser Phe Val Pro Lys Ser Pro
75 80 85
gac gca agc tct gcc ttt tcc cca gcc tcc cct gca aca cca aat gga 340
Asp Ala Ser Ser Ala Phe Ser Pro Ala Ser Pro Ala Thr Pro Asn Gly
90 95 100 105
acc aag ggc aaa aaa aaa aaa 361
Thr Lys Gly Lys Lys Lys Lys
110

<210> 92
<211> 605
<212> DNA
<213> Homo sapiens

<220>
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<222> 3..131

<221> polyA_site
<222> 591..605

<400> 92
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Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly
1 5 10 15
agc tcc cta gaa tct cct gga atg ctt aat gga cct ttc cag cac cga 95
Ser Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg
20 25 30
aat tca aga att atg act cat cgg tca gca gaa aag tgaggatacc 141
Asn Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
35 40
ttttctaacc ctacctgctt cccctgcagt ttcttcacaa tcttactctt tatattttag 201
catatgtagc ttctcaggat gttaattctg ttctctctgt gttggtgtct gagcaccag 261

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aaggtagagc caggggcact tataaaccag gagcattatt tgacaggcac ttaagaaaga 321
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gagttcgaga ccagcctggc cagcatgggtg aaaccctgtc tctactaaaa atacaaaaat 441
tagctgggtg tggttgcaca cgctgtaat ccagctacc tgggaggctg aggcaggaga 501
atcgcttgaa cttgggaggc ggagggtgca gtgagcctag attttgccat tgcactccag 561
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<221> sig_peptide
 <222> 33..80
 <223> Von Heijne matrix
 score 3.7
 seq IALTLIPMSLSRA/AG

<221> polyA_signal
 <222> 570..575

<221> polyA_site
 <222> 586..591

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Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys
                                   -5 1 5
gag ccc act cag cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg 149
Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp
                                   10 15 20
aat aag aaa ggc aac gtt ttg cag ctt cca aat ttc tgaagaaact 195
Asn Lys Lys Gly Asn Val Leu Gln Leu Pro Asn Phe
                                   25 30 35
aatctcagat tggcagttaa agtcaaaaatg ttgccaaata tttattcctt ttgcctaagt 255
ttggctaccc ggttcaattg ctttttattt ttaatgtctt gactcttcag agttcgtacc 315
tcaaaagaac aatgagaaca tttgctttgc tttctgctga atccctaata tcaacaatct 375
atacctggac tgtccagttc tctctctgtg ctatcttctc ttctatccaa gtagaatgta 435
tgccaggagc tccttccttc tagcaatttc tactaaaatg tccaagtaga atgtttcctt 495
ttacaatcaa attactgtat ttattaattt gctagaatcc agtaaatacat tttggtagct 555
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<210> 94
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 <212> DNA
 <213> Homo sapiens

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<221> sig_peptide
 <222> 184..237
 <223> Von Heijne matrix
 score 3.5
 seq LLGLELSEAEIG/AD

<221> polyA_signal
 <222> 1119..1124

<221> polyA_site
 <222> 1139..1150

<400> 94
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 gatactgggc aaagtttccc acgttgagggg tctcgaggac gcctagatct ctttcccagg 180
 gcc atg gcg aac ccg aag ctg ctg gga ctg gag cta agc gag gcg gag 228
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
 -15 -10 -5
 gcg atc ggt gct gat tcg gcg cga ttt gag gag ctg ctg ctg cag gcc 276
 Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
 1 5 10
 tcg aag gag ctc cag caa gcc cag aca acc aga cca gaa tcg aca caa 324
 Ser Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln
 15 20 25
 atc cag cct cag cct ggt ttc tgc ata aag acc aac tcc tcg gaa ggg 372
 Ile Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly
 30 35 40 45
 aag gtt ttc atc aac atc tgc cac tcc ccc tct atc cct cct ccc gcc 420
 Lys Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala
 50 55 60
 gac gtg acc gag gag gag ctg ctt cag atg cta gag gag gac caa gct 468
 Asp Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala
 65 70 75
 ggg ttt cgc atc ccc atg agt ctg gga gag cct cat gca gaa ctg gat 516
 Gly Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp
 80 85 90
 gca aaa ggc cag gga tgt acc gcc tac gac gta gct gtc aac agc gac 564
 Ala Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp
 95 100 105
 ttc tac cgg agg atg cag aac agc gat ttc ttg cgg gag ctc gtg atc 612
 Phe Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile
 110 115 120 125
 acc atc gcc agg gag ggc ctt gag gac ata tac aac ttg cag ctg aat 660
 Thr Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn
 130 135 140
 ccg gaa tgg cgc atg atg aag aac cgg cca ttc atg ggc tcc atc tcg 708
 Pro Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser
 145 150 155
 cag cag aac atc cgc tcg gag cag cgt cct cgg atc cag gag ctg ggg 756
 Gln Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly
 160 165 170
 gac ctg tac acg ccc gcc ccc ggg aga gct gag tca ggg cct gaa aag 804
 Asp Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys
 175 180 185
 cct cac ctg aac ctg tgg ctg gaa gcc ccc gac ctc ctc ttg gcc gaa 852
 Pro His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu
 190 195 200 205
 gtt gac ctc ccc aaa ctg gat gga gcc ctg ggg ctg tcg ctg gag atc 900
 Val Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile
 210 215 220
 ggg aga acc gcc tgg tgatgggggg cccccagcag ctgtatcatc tagacgctta 955

Gly Arg Thr Ala Trp

225

tatcccgccg	cagatcaact	ctcatgagag	caaggcagcc	ttccaccgga	agagaaagca	1015
attaatgggtg	gccatgccgc	ttctgccggt	gccttcttga	tcagggtgtc	tccttgtgct	1075
tctgagatgt	ggagaagagg	ctgctggctt	ccctaaaagt	tgaaataaaa	gatttttgcc	1135
tttaaaaaaa	aaaaa					1150

<210> 95

<211> 1513

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..1116

<221> sig_peptide

<222> 58..159

<223> Von Heijne matrix

score 4

seq IAVLYLHLYDVFG/DP

<221> polyA_signal

<222> 1486..1491

<221> polyA_site

<222> 1504..1513

<400> 95

ctgactcctg	agttctcaca	acgcttgacc	aataagattc	gggagcttct	tcagcaa	57
atg gag aga	ggc ctg aaa	tca gca gac	cct cgg gat	ggc acc ggt	tac	105
Met Glu Arg	Gly Leu Lys	Ser Ala Asp	Pro Arg Asp	Gly Thr Gly	Tyr	
	-30		-25		-20	
act ggc tgg	gca ggt att	gct gtg ctt	tac tta cat	ctt tat gat	gta	153
Thr Gly Trp	Ala Gly Ile	Ala Val Leu	Tyr Leu His	Leu Tyr Asp	Val	
	-15		-10		-5	
ttt ggg gac	cct gcc tac	cta cag tta	gca cat ggc	tat gta aag	caa	201
Phe Gly Asp	Pro Ala Tyr	Leu Gln Leu	Ala His Gly	Tyr Val Lys	Gln	
	1	5	10			
agt ctg aac	tgc tta acc	aag cgc tcc	atc acc ttc	ctt tgt ggg	gat	249
Ser Leu Asn	Cys Leu Thr	Lys Arg Ser	Ile Thr Phe	Leu Cys Gly	Asp	
15	20	25	30			
gca ggc ccc	ctg gca gtg	gcc gct gtg	cta tat cat	aag atg aac	aat	297
Ala Gly Pro	Leu Ala Val	Ala Ala Val	Leu Tyr His	Lys Met Asn	Asn	
	35	40	45			
gag aag cag	gca gaa gat	tgc atc aca	cgg cta att	cac cta aat	aag	345
Glu Lys Gln	Ala Glu Asp	Cys Ile Thr	Arg Leu Ile	His Leu Asn	Lys	
	50	55	60			
att gat cct	cat gct cca	aat gaa atg	ctc tat ggg	cga ata ggc	tac	393
Ile Asp Pro	His Ala Pro	Asn Glu Met	Leu Tyr Gly	Arg Ile Gly	Tyr	
	65	70	75			
atc tat gct	ctt ctt ttt	gtc aat aag	aac ttt gga	gtg gaa aag	act	441
Ile Tyr Ala	Leu Leu Phe	Val Asn Lys	Asn Phe Gly	Val Glu Lys	Thr	
	80	85	90			
cct caa agc	cat att cag	cag att tgt	gaa aca att	tta acc tct	gga	489
Pro Gln Ser	His Ile Gln	Gln Ile Cys	Glu Thr Ile	Leu Thr Ser	Gly	
95	100	105	110			
gaa aac cta	gct agg aag	aga aac ttc	acg gca aag	tct cca ctg	atg	537
Glu Asn Leu	Ala Arg Lys	Arg Asn Phe	Thr Ala Lys	Ser Pro Leu	Met	
	115	120	125			

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tat gaa tgg tac cag gaa tat tat gta ggg gct gct cat ggc ctg gct      585
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
      130                      135                      140
gga att tat tac tac ctg atg cag ccc agc ctt caa gtg agc caa ggg      633
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
      145                      150                      155
aag tta cat agt ttg gtc aag ccc agt gta gac tac gtc tgc cag ctg      681
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
      160                      165                      170
aaa ttc cct tct ggc aat tac cct cca tgt ata ggt gat aat cga gat      729
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
      175                      180                      185                      190
ctg ctt gtc cat tgg tgc cat ggc gcc cct ggg gta atc tac atg ctc      777
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
      195                      200                      205
atc cag gcc tat aag gta ttc aga gag gaa aag tat ctc tgt gat gcc      825
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
      210                      215                      220
tat cag tgt gct gat gtg atc tgg caa tat ggg ttg ctg aag aag gga      873
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
      225                      230                      235
tat ggg ctg tgc cac ggt tct gca ggg aat gcc tat gcc ttc ctg aca      921
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
      240                      245                      250
ctc tac aac ctc aca cag gac atg aag tac ctg tat agg gcc tgt aag      969
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
      255                      260                      265                      270
ttt gct gaa tgg tgc tta gag tat gga gaa cat gga tgc aga aca cca      1017
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
      275                      280                      285
gac acc cct ttc tct ctc ttt gaa gga atg gct ggg aca ata tat ttc      1065
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
      290                      295                      300
ctg gct gac ctg cta gtc ccc aca aaa gcc agg ttc cct gca ttt gaa      1113
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
      305                      310                      315
ctc tgaaaggata gcatgccacc tgcaactcac tgcattgaccc tttctgtata      1166
Leu
ttcaaaccga agctaagtgc ttccgttgct ttccaaggaa acaaagagtc aaactgtgga      1226
cttgattttg ttagcttttt tcagaattta tctttcattc agttcccttc cattatcatt      1286
tacttttact tagaagtatc caaggaagtc ttttaacttt aatttccatt tcttcctaaa      1346
gggagagtga gtgatatgta cagtgttttg agattgtata catatatccc agaacttgga      1406
ggaaatctta ttttaagttta tgaatataac catctgttac tgttctaaaa atgttttaaa      1466
gaaactcaat acagataaag ataaatatgt gactattaaa aaaaaaa      1513

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<210> 96
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 327..416

<221> polyA_site
 <222> 404..417

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<400> 96
tgttttgagg tgttggcatt ctctgctgat ttggctgttc ccaatgttta cattatttta      60
tcttgcacaa atggttctgt gcacttgat gtgaaatgct gtccagtttt atttttttta      120

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tgttggtatc cttggatgta caaaaaattc agaaaatgat ctctgtagat attctgtttt 180
attttggtca tctttagaag ttatcaggaa tgtgtttaaa acaagaagag aacttttcta 240
aggaatgata catagaaaag attttatttt aaaatgagtt gtaaagcttg tgtttctttg 300
ttgctgcaag ctatctgccc aagtta atg caa atg gac aca ttt ttt atg tca 353
                               1       5
                               Met Gln Met Asp Thr Phe Phe Met Ser
gaa aaa cac aca cac aca cac aca cat ata cac aca cac aca cga aaa 401
Glu Lys His Thr His Thr His Thr His Ile His Thr His Thr Arg Lys
10              15              20              25
aca aaa aaa aaa aaa a 417
Thr Lys Lys Lys Lys
              30

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<210> 97
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..398

<221> sig_peptide
 <222> 63..206
 <223> Von Heijne matrix
 score 4.9
 seq PSLAAGLLFGSLA/GL

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<400> 97
ggggccttcg tgagaccggt gcaggcctgg ggtagtctcc tgtctggaca gagaagagaa 60
aa atg cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt 107
   Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe
       -45              -40              -35
ggc tac gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa 155
Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys
       -30              -25              -20
gca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta 203
Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
       -15              -10              -5
gcc ggc ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg 251
Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp
   1              5              10              15
gtt ttc cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg 299
Val Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg
       20              25              30
ttc tac cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc 347
Phe Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala
       35              40              45
agt ttg ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc 395
Ser Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro
       50              55              60
cat tagcagaagt catgttccag ccttagactga tgaagaatta aaaatctgca 448
His
tcttccacta ttttcaatat attaagagaa ataagtgcag catttttgca tctgacattt 508
tacctaataaa aaaagacacc aaacttgga gagaggtgga aaatcagtca tgattacaaa 568
cctacagagg tggcgagtat gtaacacaag agctt 603

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<210> 98

<211> 522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..163

<221> polyA_signal
 <222> 488..493

<221> polyA_site
 <222> 511..522

<400> 98
 c gag att gcg ggc tat ggc gcc gaa ggt ttt tcg tca gta ctg gga tat 49
 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15
 ccc cga tgg cac cga ttg cca ccg caa agc cta cag cac cac cag tat 97
 Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 tgc cag cgt cgc tgg cct gac cgc cgc tgc cta cag agt cac act caa 145
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 tcc tcc ggg cac ctt cct nntgaaggag tggctaagggt tggacaatac 193
 Ser Ser Gly His Leu Pro
 50
 acgttcactg cagctgctgt cggggccgtg tttggcctca ccacctgcat cagcgcccat 253
 gtccgcgaga agcccgacga cccctgaac tacttccccg gtggctgcgc cnggaggcct 313
 gactctggga gcacgcacgc acaactacgg gattggcgcc gccgcctgcg tgtactttgg 373
 catagcggcc tccctgggtca agatgggccc gctggagggc tgggaggtgt ttgcaaaacc 433
 caaggtgtga gccctgtgcc tgccgggacc tccagcctgc agaatgcgtc cagaaataaa 493
 ttctgtgtct gtgtgtgaaa aaaaaaaaaa 522

<210> 99
 <211> 956
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..465

<221> sig_peptide
 <222> 13..75
 <223> Von Heijne matrix
 score 3.9
 seq PVAVTAAVAPVLS/IN

<400> 99
 ngagtcggga aa atg gct gcg agt acn tcn atg gnc ccg gtg gct gtg acg 51
 Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr
 -20 -15 -10
 gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg 99
 Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
 -5 1 5
 cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag 147
 Arg Glu Ile Lys Lys Gln Leu Leu Ile Ala Gly Leu Thr Arg Glu
 10 15 20
 cgg ggc cta cta cac agt agc aaa tgg tcg gcg gag ttg gct ttc tct 195

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Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
25          30          35          40
ctc cct gca ttg cct cnt ggc cag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr
          45          50          55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
          60          65          70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
          75          80          85
aat agc aag aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ser Lys Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
          90          95          100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
          105          110          115          120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
          125          130
gaatgaatgt actttatata tagcaataat aaaaaaaaga tatcataaat aaagttaaaa      545
aggatggtag agaagaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atttatttac tttagggtat ataaggttct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattta tcatgtttat      725
agtatattta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agnaaaccaa ctttaatactg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acntnnccatt tcctagtaca ggttgagtat cccttatttg a          956

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<210> 100

<211> 1041

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 20..703

<221> sig_peptide

<222> 20..94

<223> Von Heijne matrix

score 3.9

seq ATVGLLMLGVTLF/NS

<221> polyA_signal

<222> 1000..1005

<221> polyA_site

<222> 1023..1041

<400> 100

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cagggtcctg catcctacc atg tcg atg gct gtg gaa acc ttt ggc ttc ttc      52
          Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe
          -25          -20          -15
atg gca act gtg ggg ctg ctg atg ctg ggg gtg act ctg cca aac agc      100
Met Ala Thr Val Gly Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser
          -10          -5          1
tac tgg cga gtg tcc act gtg cac ggg aac gtc atc acc acc aac acc      148
Tyr Trp Arg Val Ser Thr Val His Gly Asn Val Ile Thr Thr Asn Thr
          5          10          15

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atc ttc gag aac ctc tgg ttt agc tgt gcc acc gac tcc ctg ggc gtc 196
Ile Phe Glu Asn Leu Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val
20 25 30
tac aac tgc tgg gag ttc ccg tcc atg ctg gcc ctc tct ggg tat att 244
Tyr Asn Cys Trp Glu Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile
35 40 45 50
cag gcc tgc cgg gca ctc atg atc acc gcc atc ctc ctg ggc ttc ctc 292
Gln Ala Cys Arg Ala Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu
55 60 65
ggc ctc ttg cta ggc ata gcg ggc ctg cgc tgc acc aac att ggg ggc 340
Gly Leu Leu Leu Gly Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly
70 75 80
ctg gag ctc tcc agg aaa gcc aag ctg gcg gcc acc gca ggg gcc ccc 388
Leu Glu Leu Ser Arg Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro
85 90 95
cac att ctg gcc ggt atc tgc ggg atg gtg gcc atc tcc tgg tac gcc 436
His Ile Leu Ala Gly Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala
100 105 110
ttc aac atc acc cgg gac ttc ttc gac ccc ttg tac ccc gga acc aag 484
Phe Asn Ile Thr Arg Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys
115 120 125 130
tac gag ctg ggc ccc gcc ctc tac ctg ggg tgg agc gcc tca ctg atc 532
Tyr Glu Leu Gly Pro Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile
135 140 145
tcc atc ctg ggt ggc ctc tgc ctc tgc tcc gcc tgc tgc tgc ggc tct 580
Ser Ile Leu Gly Gly Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser
150 155 160
gac gag gac cca gcc gcc agc gcc cgg cgg ccc tac cag gct cca gtg 628
Asp Glu Asp Pro Ala Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val
165 170 175
tcc gtg atg ccc gtc gcc acc tcg gac caa gaa ggc gac agc agc ttt 676
Ser Val Met Pro Val Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe
180 185 190
ggc aaa tac ggc aga aac gcc tac gtg tagcagctct ggcccgtggg 723
Gly Lys Tyr Gly Arg Asn Ala Tyr Val
195 200
ccccgctgtc ttccactgc cccaaggaga ggggacctgg ccggggccca ttcccctata 783
gtaacctcag gggccggcca cgccccgctc ccgtagcccc gccccggcca cgccccctg 843
tcttgactc tcatggcccc tccaggccaa gaactgctct tgggaagtgc catatctccc 903
ctctgaggct ggatccctca tcttctgacc ctgggttctg ggctgtgaag gggacgggtgt 963
ccccgcacgt ttgtattgtg tataaatata ttcattaata aatgcatatt gtgaccgtta 1023
aaaaaaaaa aaaaaaaaa 1041

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<210> 101

<211> 558

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 103..294

<221> sig_peptide

<222> 103..243

<223> Von Heijne matrix

score 5.9

seq TWLGLLSFQNLHC/FP

<400> 101

ttcccatggt ttagaagcat aacctgtaat gtaatgcaag tcccctaact ccctggttgc 60

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taacattaac ttccttaagt aataatcaat gaaagaaatt ct atg cat ggt ttt      114
                                   Met His Gly Phe
                                   -45
gaa ata ata tcc ttg aaa gag gaa tca cca tta gga aag gtg agt cag      162
Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly Lys Val Ser Gln
-40                                -35                                -30
ggt cct ttg ttt aat gtg act agt ggc tca tca tca cca gtg acc tgg      210
Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser Pro Val Thr Trp
-25                                -20                                -15
ttg ggc cta ctc tcc ttc cag aac ctg cat tgc ttc cca gac ctc ccc      258
Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe Pro Asp Leu Pro
-10                                -5                                1                                5
act gag atg cct cta aga gcc aaa gga gtc aac act tgagcctagg      304
Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
10                                15
gtgggctaca acaaaagatt ctaatttacc ttgcttcac taggtccagg ccccaagtag      364
cttgctgaag gaacttaaaa agtagctgtt atttattgta ttgtataagc taaaaacatt      424
tatttttgtt gaatcgaaac aattccatgt agcaatcttt tttctgttca cgggtgttgt      484
gatagaacct taaattccgc aagcatcagt tttttgaaaa aatgggaatt gaccggatag      544
taacaggcaa agtt      558

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<210> 102

<211> 730

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 81..518

<221> sig_peptide

<222> 81..173

<223> Von Heijne matrix

score 3.9

seq ILFHGVFYAGGFA/IV

<400> 102

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ctcgtcatgc tctttgtagc gtggtgcttc tgttctcac aggacaactt gcctttgatg      60
attttcaaga gagttgtgct atg atg tgg caa aag tat gca gga agc agg cgg      113
                                   Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg
                                   -30                                -25
tca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc      161
Ser Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
-20                                -15                                -10                                -5
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg      209
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
1                                5                                10
gct tta tat tac aag ttg gca gtg gag cag ctg cag agc cat ccc gag      257
Ala Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu
15                                20                                25
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc      305
Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
30                                35                                40
atc gac agg gaa aac ttc gtg gac att gtt gat gcc aag ttg aag att      353
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile
45                                50                                55                                60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc      401
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
65                                70                                75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag      449

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Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
 80 85 90
 ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac 497
 Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
 95 100 105
 ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt 548
 Gly Asp Glu Val Lys Lys Glu
 110 115
 ctagtccatc cttccctcat ctctaccata tggccactgg ggtgggtggcc catctcagtg 608
 acagacactc ctgcaaccca gttttccagc caccagtggg atgatggat gtgccagcac 668
 atggtaat tgggtgaatt ctaacttggg cacaacgaat gctatttgtc atttttaaac 728
 tg 730

<210> 103
 <211> 1098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..326

<221> polyA_signal
 <222> 1066..1071

<221> polyA_site
 <222> 1087..1098

<400> 103
 ctccctttga atgagagaaa ctaaccgct tccgaagccc ctgaaagaca ctgctccttc 60
 ctctc atg gag ttg gct ccg aca gcc cgt ctg cca cca ggc cat ggt tcc 110
 Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser
 1 5 10 15
 ttg ccc cat ggt gtc ctg gga ccc aga gca aca gga tct gtc acc cac 158
 Leu Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His
 20 25 30
 ctc tct ctt ctc ccc cag atc aag caa cgt gcc tca gag gct ttg ccc 206
 Leu Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro
 35 40 45
 gaa ttg ctt cgt cct gtc acc ccc atc acc aat ttt gag ggc agc cag 254
 Glu Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln
 50 55 60
 tct cag gac cac agt gga atc ttt ggc ctg gta aca aac ctg gaa gag 302
 Ser Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu
 65 70 75
 ctg gag gtg gac gat tgg gag ttc tgagcctctg caaactgtgc gcattctcca 356
 Leu Glu Val Asp Asp Trp Glu Phe
 80 85
 gccagggatg cagaggccac ccagaggccc ttcctgaggg ccggccacat tcccgccttc 416
 ctgggcagat tgggtagaaa ggacattctt ccaggaaagt tgactgctgg ctgattggga 476
 aagaaaatcc tggagagata cttcactgct ccaaggcttt tgagacacaa gggaatctca 536
 acaaccaggg atcaggaggg tccaaagccg acattcccag tcctgtgagc tcagggtgacc 596
 tctccgcag aagagagatg ctgctctggc cctgggagct gaattccaag cccagggttt 656
 ggctccttaa acccgaggac cgccacctct tccagtgct tgcgaccagc ctcatcttac 716
 ttaactttgc tctcagatgc ctcatgtct ataggtcagt gaaagggcga gtagtaagct 776
 gctgctcct cttccctcag acctctcct cataattcca gagaaggcca tttctgtctt 836
 ttaagcaca gactaaggct ggaacagtc atccttatcc ctcttctggc ttgggcccctg 896
 acacctaagt ctttcccacg gtttatgtgt gtgctcatt cctttcccac caagaatcca 956
 tcttagcgcc tctgcccagc tgccctgggt ctttctccaa gggccatcag tgtcttgctt 1016
 agcttgaggg cttaagtcct tatgtgtgt tagtttcgtt gtcagaacaa attaaaattt 1076

tcagagacgc aaaaaaaaaa aa

1098

<210> 104

<211> 346

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 170..289

<221> sig_peptide

<222> 170..250

<223> Von Heijne matrix

score 3.6

seq LLLLLITPSPSPL/LF

<400> 104

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ccatttgagc cccaccacgg aggttatgtg gtcccaaaag gaatgatggc caagcaatta    60
atatttcctc ctagttctta gcttgcttct gcattgattg gctttacaca actggcattt    120
agtctgcatt acacaaatag acactaattt atttggaaca agcagcaaa atg aga act    178
                                   Met Arg Thr
                                   -25
```

```
tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act ctg ctt cta    226
Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr Leu Leu Leu
                                   -20          -15          -10
```

```
atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt ctg tcc ctc    274
Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly Leu Ser Leu
                                   -5          1          5
```

```
aga tca gca atg tct tagccctct cctctcttcc attccttcc gttggtactc    329
Arg Ser Ala Met Ser
10
```

```
atttcttcta actttta    346
```

<210> 105

<211> 685

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..497

<221> polyA_signal

<222> 650..655

<221> polyA_site

<222> 663..685

<400> 105

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aagttctgcg ctggtcggcg gagtagcaag tggcc atg ggg agc ctc agc ggt    53
                                   Met Gly Ser Leu Ser Gly
                                   1          5
```

```
ctg cgc ctg gca gca gga agc tgt ttt agg tta tgt gaa aga gat gtt    101
Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val
                                   10          15          20
```

```
tcc tca tct cta agg ctt acc aga agc tct gat ttg aag aga ata aat    149
Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn
```

```

      25              30              35
gga ttt tgc aca aaa cca cag gaa agt ccc gga gct cca tcc cgc act 197
Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr
      40              45              50
tac aac aga gtg cct tta cac aaa cct acg gat tgg cag aaa aag atc 245
Tyr Asn Arg Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile
      55              60              65              70
ctc ata tgg tca ggt cgc ttc aaa aag gaa gat gaa atc cca gag act 293
Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu Asp Glu Ile Pro Glu Thr
      75              80              85
gtc tgc ttg gag atg ctt gat gct gca aag aac aag atg cga gtg aag 341
Val Ser Leu Glu Met Leu Asp Ala Ala Lys Asn Lys Met Arg Val Lys
      90              95              100
agc agc tat cta atg att gcc ctg acg gtg gta gga tgc atc ttc atg 389
Ser Ser Tyr Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met
      105              110              115
gtt att gag ggc aag aag gct gcc caa aga cac gag act tta aca agc 437
Val Ile Glu Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser
      120              125              130
ttg aac tta gaa aag aaa gct cgt ctg aaa gag gaa gca gct atg aag 485
Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys Glu Glu Ala Ala Met Lys
      135              140              145              150
gcc aaa aca gag tagcagaggt atccgtgttg gctggatttt gaaaatccag 537
Ala Lys Thr Glu
gaattatggt ataacgtgcc tgtattaaaa aggatgtggt atgaggatcc atttcataaaa 597
gtatgatttg cccaaacctg taccatttcc gtatttctgc cgtagaagta gaaataaatt 657
ttcttaaaaa aaaaaaaaaa aaaaaaaaaa 685

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<210> 106

<211> 554

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..320

<221> polyA_signal

<222> 539..544

<221> polyA_site

<222> 542..554

<400> 106

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aaccgtcgtg gggaagg atg gtg tgc gaa aaa tgt gaa aag aaa ctt ggt 50
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly
      1              5              10
act gtt atc act cca gat aca tgg aaa gat ggt gct agg aat acc aca 98
Thr Val Ile Thr Pro Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr
      15              20              25
gaa agt ggt gga aga aag ctg aat aaa aat aaa gct ttg act tca aaa 146
Glu Ser Gly Gly Arg Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys
      30              35              40
aaa gca aga ttt gat cca tat gga aag aat aag ttc tcc act tgt aga 194
Lys Ala Arg Phe Asp Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg
      45              50              55
att tgt aaa agt tct gtg cac caa cca ggt tct cat tac tgc cag ggc 242
Ile Cys Lys Ser Ser Val His Gln Pro Gly Ser His Tyr Cys Gln Gly
      60              65              70              75
tgt gcc tac aaa aaa ggc atc tgt gcg atg tgt ggn aaa aaa gtt ttg 290

```

Cys Ala Tyr Lys Lys Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu
 80 85 90
 gat acc aaa aac tac aag caa aca tct gtc tagatgtatt gatggaattt 340
 Asp Thr Lys Asn Tyr Lys Gln Thr Ser Val
 95 100
 ctggctttct aaatgatttt actttctgcc ttgaattttc aaggcataga tgtcaactta 400
 cagaataaca tgttttaaga taattaagtt taaaccagag aatttgattg ttactcattt 460
 tgctctcatg ttctaaacag caacagtgt actagtcttt tggtgtaaat gggtattttc 520
 cttataagaa ttttaagaac taaaaaaaaa aaaa 554

<210> 107
 <211> 1678
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 71..1438

<221> sig_peptide
 <222> 71..136
 <223> Von Heijne matrix
 score 3.5
 seq AAPVAAGLGPVIS/RP

<221> polyA_signal
 <222> 1644..1649

<221> polyA_site
 <222> 1665..1678

<400> 107
 ccgacttcca gaggagcgct gtgcacgtgg agaagagcgg ggactcggcg accctgccct 60
 cccgaccctc atg ttc gaa gag cct gag tgg gcc gag gcg gcc cca gta 109
 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val
 -20 -15 -10
 gcc gcg ggc ctt ggg ccc gta atc tca cga cct ccg cct gcg gcc tcc 157
 Ala Ala Gly Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser
 -5 1 5
 tcg caa aac aag ggc tcc aag cgc cgc cag ctc ttg gcc aca tta cgg 205
 Ser Gln Asn Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg
 10 15 20
 gcc cta gag gca gca tct ctt tcc cag cat ccc ccc agc cta tgt ata 253
 Ala Leu Glu Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile
 25 30 35
 agt gac tct gag gag gag gag gag gaa agg aag aag aaa tgc ccc aaa 301
 Ser Asp Ser Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys
 40 45 50 55
 aag gca tca ttt gcc agt gcc tct gct gaa gta ggg aag aaa ggg aag 349
 Lys Ala Ser Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys
 60 65 70
 aag aaa tgt caa aaa cag ggc cca cct tgc agt gac tct gag gaa gaa 397
 Lys Lys Cys Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu
 75 80 85
 gta gaa agg aag aag aaa tgc cac aaa cag gct ctt gtt ggc agt gac 445
 Val Glu Arg Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp
 90 95 100
 tct gct gaa gat gag aaa aga aag agg aaa tgc cag aaa cat gcc cct 493
 Ser Ala Glu Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro
 105 110 115

ata aat tca gcc cag cac ctg gac aat gtt gac caa aca ggt ccc aaa	541
Ile Asn Ser Ala Gln His Leu Asp Asn Val Asp Gln Thr Gly Pro Lys	
120 125 130 135	
gcc tgg aag ggt agt act aca aat gat cca cca aag caa agc cct ggg	589
Ala Trp Lys Gly Ser Thr Thr Asn Asp Pro Pro Lys Gln Ser Pro Gly	
140 145 150	
tcc act tcc cct aaa ccc cct cat aca tta agc cgc aag cag tgg cgg	637
Ser Thr Ser Pro Lys Pro Pro His Thr Leu Ser Arg Lys Gln Trp Arg	
155 160 165	
aac cgg caa aag aat aag aga aga tgt aag aac aag ttt cag cca cct	685
Asn Arg Gln Lys Asn Lys Arg Arg Cys Lys Asn Lys Phe Gln Pro Pro	
170 175 180	
cag gtg cca gac cag gcc cca gct gag gcc ccc aca gag aag aca gag	733
Gln Val Pro Asp Gln Ala Pro Ala Glu Ala Pro Thr Glu Lys Thr Glu	
185 190 195	
gtg tct cct gtt ccc agg aca gac agc cat ggg gct cgg gca ggg gct	781
Val Ser Pro Val Pro Arg Thr Asp Ser His Gly Ala Arg Ala Gly Ala	
200 205 210 215	
ttg cga gcc cgc atg gca cag cgg ctg gat ggg gcc cga ttt cgc tac	829
Leu Arg Ala Arg Met Ala Gln Arg Leu Asp Gly Ala Arg Phe Arg Tyr	
220 225 230	
ctc aat gaa cag ttg tac tca ggg ccc agc agt gct gca cag cgt ctc	877
Leu Asn Glu Gln Leu Tyr Ser Gly Pro Ser Ser Ala Ala Gln Arg Leu	
235 240 245	
ttc cag gaa gac cct gag gct ttt ctt ctc tac cac cgc ggc ttc cag	925
Phe Gln Glu Asp Pro Glu Ala Phe Leu Leu Tyr His Arg Gly Phe Gln	
250 255 260	
agc caa gtg aag aag tgg cca ctg cag cca gtg gac cgc atc gcc agg	973
Ser Gln Val Lys Lys Trp Pro Leu Gln Pro Val Asp Arg Ile Ala Arg	
265 270 275	
gat ctt cgc cag cgg cct gca tcc cta gtg gtg gct gac ttc ggc tgt	1021
Asp Leu Arg Gln Arg Pro Ala Ser Leu Val Val Ala Asp Phe Gly Cys	
280 285 290 295	
ggg gat tgc cgc ttg gct tca agt atc cgg aac cct gtg cat tgc ttt	1069
Gly Asp Cys Arg Leu Ala Ser Ser Ile Arg Asn Pro Val His Cys Phe	
300 305 310	
gac ttg gct tct ctg gac cct agg gtc act gtg tgt gac atg gcc cag	1117
Asp Leu Ala Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln	
315 320 325	
gtt cct ttg gag gat gag tct gtg gat gtg gct gtg ttt tgc ctt tca	1165
Val Pro Leu Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser	
330 335 340	
ctg atg gga acc aac atc agg gac ttc cta gag gag gca aat aga gta	1213
Leu Met Gly Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val	
345 350 355	
ctg aag cca ggg ggt ctc ctg aaa gtg gct gag gtc agc agc cgc ttt	1261
Leu Lys Pro Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe	
360 365 370 375	
gag gat gtt cga acc ttt ctg cgg gct gtg acc aag cta ggc ttc aag	1309
Glu Asp Val Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys	
380 385 390	
att gtc tcc aag gac ctg acc aac agc cat ttc ttc ttg ttt gat ttc	1357
Ile Val Ser Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe	
395 400 405	
caa aag act ggg ccc cct ctg gta ggg ccc aag gct cag ctt tca ggc	1405
Gln Lys Thr Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly	
410 415 420	
ctg cag ctt cag cca tgt ctc tac aag cgc agg tgacctctgg atcttccttg	1458
Leu Gln Leu Gln Pro Cys Leu Tyr Lys Arg Arg	
425 430	
agaggggagg cagatctcaa actccaggct cagaactgtg aagactgttt ccggcctggc	1518
tgtgagccaa gacctgggtc ctggtggacc ctgaggacaa agtgtgataa aacctctggc	1578

tcagacttgcc tctactgaag gcttcttgggt tataagatgc ataaagtcac tggggctagc 1638
 taaacaataa agagtttatt gtgaggaaaa aaaaaaaaaa 1678

<210> 108
 <211> 494
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..318

<221> sig_peptide
 <222> 25..75
 <223> Von Heijne matrix
 score 7.4
 seq FFLLLQFFLRIDG/VL

<221> polyA_signal
 <222> 452..457

<221> polyA_site
 <222> 482..494

<400> 108
 aggctgagtg tgaagattag agta atg cct tct agc ttt ttc ctg ctg ttg 51
 Met Pro Ser Ser Phe Phe Leu Leu
 -15 -10
 cag ttt ttc ttg aga att gat ggg gtg ctt atc aga atg aat gac acg 99
 Gln Phe Phe Leu Arg Ile Asp Gly Val Leu Ile Arg Met Asn Asp Thr
 -5 1 5
 aga ctt tac cat gag gct gac aag acc tac atg tta cga gaa tat acg 147
 Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr Met Leu Arg Glu Tyr Thr
 10 15 20
 tca cga gaa agc aaa att tct agt ttg atg cat gtt cca cct tcc ctc 195
 Ser Arg Glu Ser Lys Ile Ser Ser Leu Met His Val Pro Pro Ser Leu
 25 30 35 40
 ttc acg gaa cct aat gaa ata tcc cag tat tta cca ata aag gaa gca 243
 Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr Leu Pro Ile Lys Glu Ala
 45 50 55
 gtt tgt gag aag cta ata ttt cca gaa aga att gat cct aac cca gca 291
 Val Cys Glu Lys Leu Ile Phe Pro Glu Arg Ile Asp Pro Asn Pro Ala
 60 65 70
 gac tca caa aaa agt aca caa gtg gaa taaaatgtga tacaacatat 338
 Asp Ser Gln Lys Ser Thr Gln Val Glu
 75 80
 actcactatg gaatctgact ggacaccttg gctatttgta aggggttatt tttattatga 398
 gaattaattg ccttggttat gtacagatgt tctgtagcct taaaggaaaa aaaaataaag 458
 atcgttacag gcaggtttca ctcaaaaaaa aaaaac 494

<210> 109
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..332

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<221> sig_peptide
<222> 84..170
<223> Von Heijne matrix
      score 5.2
      seq PCYYLGLGFQRALA/SV
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<221> polyA_site
<222> 702..714
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<400> 109		
cctatctctt ctgctggctg ggctcaatgc cgcgggtgag cgttcggccg aggctgctcc		60
tacccttgag tgatgtgcct tga atg acg ctg ctt tca ttc gct gct ttc acg		113
Met Thr Leu Leu Ser Phe Ala Ala Phe Thr		
-25	-20	
gct gct ttc tcc gtc ctc ccc tgt tac tac ctt ggg ctg ttt cag cgg		161
Ala Ala Phe Ser Val Leu Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg		
-15	-10	-5
gcg ctc gcg tcg gtc ttc gac cca ctt tgc gtt tgt tca cgt gtg ctc		209
Ala Leu Ala Ser Val Phe Asp Pro Leu Cys Val Cys Ser Arg Val Leu		
1	5	10
ccg aca cct gta tgt acc ttg gtc gca aca caa gcc gaa aaa ata tta		257
Pro Thr Pro Val Cys Thr Leu Val Ala Thr Gln Ala Glu Lys Ile Leu		
15	20	25
gag aat ggg ccc tgt cca acc aag gag gcg gcc cag ctt gtc ggg aag		305
Glu Asn Gly Pro Cys Pro Thr Lys Glu Ala Ala Gln Leu Val Gly Lys		
30	35	40
ggc agc gtt tcc gcc aga aat gct tcg tgaaaggcac ttgagggacc		352
Gly Ser Val Ser Ala Arg Asn Ala Ser		
50		
ttagcagcat cctcaacagg ccttgtaggg aatgccagaa gaagcagtc ttggccgggc		412
ggggtggctc atgcctgtgg tcccagcact ttgggaggcc ggggcgggcg gatcacctga		472
ggtcgggagg tccagaccag cctgaccgac atggagaaac cccgtctnta ctagaaatac		532
aaaactagcc ggggtgtggtg gcgcatgcct gtagtcccag ctactcgga ggggtaggca		592
ggagacgttc ttgaaccgg gaggcggagt ttgtggtgag ccgagatcgc gccattgcac		652
tccagcctgg gcatgccaaag agcgaaatc cgtctcaaaa aaaaaaaaga aaaaaaaaaa		712
aa		714

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<210> 110
<211> 805
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 32..718
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<221> sig_peptide
<222> 32..100
<223> Von Heijne matrix
      score 7.4
      seq VLLLLAALPPVLLP/GA
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<221> polyA_signal
<222> 770..775
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<221> polyA_site
<222> 793..805
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 $\langle 400 \rangle$ 110

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cctcttttcag cccgggatcg ccccagcagg g atg ggc gac aag atc tgg ctg      52
Met Gly Asp Lys Ile Trp Leu
-20
ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg cct      100
Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro
-15 -10 -5
ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt acc      148
Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr
1 5 10 15
ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg aag      196
Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys
20 25 30
gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta gat      244
Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp
35 40 45
att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt gaa      292
Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu
50 55 60
caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt gat      340
Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp
65 70 75 80
tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag gtg      388
Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val
85 90 95
att ttc ttt gaa tta atc ctg gat aat atg gga gaa cag gca caa gaa      436
Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
100 105 110
caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat atg      484
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp Met
115 120 125
aaa ctg gaa gac atc ctg gaa tcc atc agc agc atc aag tcc aga cta      532
Lys Leu Glu Asp Ile Leu Glu Ser Ile Ser Ser Ile Lys Ser Arg Leu
130 135 140
agc aaa agt ggg cac ata caa att ctg ctt aga gca ttt gaa gct cgt      580
Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe Glu Ala Arg
145 150 155 160
gat cga aac ata caa gaa agc aac ttt gat aga gtc aat ttc tgg tct      628
Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val Asn Phe Trp Ser
165 170 175
atg gtt aat tta gtg gtc atg gtg gtg gtg tca gcc att caa gtt tat      676
Met Val Asn Leu Val Val Met Val Val Val Ser Ala Ile Gln Val Tyr
180 185 190
atg ctg aag agt ctg ttt gaa gat aag agg aaa agt aga act      718
Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr
195 200 205
taaaactcca aactagagta cgtaacattg aaaaatgagg cataaaaatg caataaactg      778
ttacagtcaa gaccacaaaaa aaaaaaa      805

```

<210> 111

<211> 787

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26..481

<221> sig_peptide

<222> 26..88

<223> Von Heijne matrix

score 4.4
seq AVASSFFCASLFS/AV

<221> polyA_signal
<222> 755..760

<221> polyA_site
<222> 775..787

<400> 111
gacagcctgg ataaaggctc acttg atg gct cag ttg gga gca gtt gtg gct 52
Met Ala Gln Leu Gly Ala Val Val Ala
-20 -15
gtg gct tcc agt ttc ttt tgt gca tct ctc ttc tca gct gtg cac aag 100
Val Ala Ser Ser Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys
-10 -5 1
ata gaa gag gga cat att ggg gta tat tac aga ggc ggt gcc ctg ctg 148
Ile Glu Glu Gly His Ile Gly Val Tyr Tyr Arg Gly Gly Ala Leu Leu
5 10 15 20
act tcg acc agc ggc cct ggt ttc cat ctc atg ctc cct ttc atc aca 196
Thr Ser Thr Ser Gly Pro Gly Phe His Leu Met Leu Pro Phe Ile Thr
25 30 35
tca tat aag tct gtg cag acc aca ctc cag aca gat gag gtg aag aat 244
Ser Tyr Lys Ser Val Gln Thr Thr Leu Gln Thr Asp Glu Val Lys Asn
40 45 50
gta cct tgt ggg act agt ggt ggt gtg atg atc tac ttt gac aga att 292
Val Pro Cys Gly Thr Ser Gly Gly Val Met Ile Tyr Phe Asp Arg Ile
55 60 65
gaa gtg gtg aac ttc ctg gtc ccg aac gca gtg cat gat ata gtg aag 340
Glu Val Val Asn Phe Leu Val Pro Asn Ala Val His Asp Ile Val Lys
70 75 80
aac tat act gct gac tat gac aag gcc ctc atc ttc aac aag atc cac 388
Asn Tyr Thr Ala Asp Tyr Asp Lys Ala Leu Ile Phe Asn Lys Ile His
85 90 95 100
cac gaa ctg aac cag ttc tgc agt gtg cac acg ctt caa gag gtc tac 436
His Glu Leu Asn Gln Phe Cys Ser Val His Thr Leu Gln Glu Val Tyr
105 110 115
att gag ctg ttt gga ctg gaa aat gat ttt tcc cag gaa tct tca 481
Ile Glu Leu Phe Gly Leu Glu Asn Asp Phe Ser Gln Glu Ser Ser
120 125 130
taaaagggac cctgagcaag aacatttttc atagcagaca ggaggactca tccacatcgc 541
cagcaatcat aattaagcaa accgcctttt gcaccattta agatttagga aatcatccaa 601
attactttta atgtttctgc agtagaaaat gaatctaaat tcattttata gggttttag 661
tcttttatct gttttggatt cactgtgctt ttaagaaaaa gtttggtaaat ttgccgttga 721
tttttctttt taacctcaaa ctaatagaat tttataaaat attaattttc tccaaaaaaa 781
aaaaaa 787

<210> 112
<211> 569
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..562

<221> sig_peptide
<222> 26..187
<223> Von Heijne matrix
score 4.1

seq AVVAAAARTGSEA/RV

<400> 112

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agaaacaggt ctgggctaca aaagt atg gcc gct tct gag gcg gcg gtg gtg      52
                               Met Ala Ala Ser Glu Ala Ala Val Val
                               -50
tct tcg ccg tct ttg aaa aca gac aca tcc cct gtc ctt gaa act gca      100
Ser Ser Pro Ser Leu Lys Thr Asp Thr Ser Pro Val Leu Glu Thr Ala
-45                               -40                               -35                               -30
gga acg gtc gca gca atg gct gcg acc ccg tca gca agg gct gca gcc      148
Gly Thr Val Ala Ala Met Ala Ala Thr Pro Ser Ala Arg Ala Ala Ala
                               -25                               -20                               -15
gcg gtg gtt gcg gcc gcg gcc agg acc gga tcc gaa gcc agg gtc tcc      196
Ala Val Val Ala Ala Ala Ala Arg Thr Gly Ser Glu Ala Arg Val Ser
                               -10                               -5                               1
aag gcc gct ttg gct acc aag ctg ctg tcc ttg agc ggc gtg ttc gcc      244
Lys Ala Ala Leu Ala Thr Lys Leu Leu Ser Leu Ser Gly Val Phe Ala
5                               10                               15
gtg cac aag ccc aaa ggg ccc act tca gcc gag ctg ctg aat cgg ttg      292
Val His Lys Pro Lys Gly Pro Thr Ser Ala Glu Leu Leu Asn Arg Leu
20                               25                               30                               35
aag gag aag ctg ctg gca gaa gct gga atg cct tct cca gaa tgg acc      340
Lys Glu Lys Leu Leu Ala Glu Ala Gly Met Pro Ser Pro Glu Trp Thr
                               40                               45                               50
aag agg aaa aag cag act ttg aaa att ggg cat gga ggg act cta gac      388
Lys Arg Lys Lys Gln Thr Leu Lys Ile Gly His Gly Gly Thr Leu Asp
                               55                               60                               65
agc gca gcc cga gga gtt ctg gtt gtt gga att gga agc gga aca aaa      436
Ser Ala Ala Arg Gly Val Leu Val Val Gly Ile Gly Ser Gly Thr Lys
70                               75                               80
atg ttg acc agt atg ttg tca ggg tcc aag agg tat act gcc att gga      484
Met Leu Thr Ser Met Leu Ser Gly Ser Lys Arg Tyr Thr Ala Ile Gly
85                               90                               95
gaa ctg ggg aaa gct act gat aca cta gat tct acg ggg aag gta aca      532
Glu Leu Gly Lys Ala Thr Asp Thr Leu Asp Ser Thr Gly Lys Val Thr
100                               105                               110                               115
gaa gaa aaa cct tac ggt atg aac ctc atc taagtag      569
Glu Glu Lys Pro Tyr Gly Met Asn Leu Ile
                               120                               125

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<210> 113

<211> 893

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..810

<221> sig_peptide

<222> 4..279

<223> Von Heijne matrix

score 6.8

seq AVMLYTWRSCSRA/IP

<221> polyA_signal

<222> 858..863

<221> polyA_site

<222> 881..893

<400> 113

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gcc atg atc acg cac gtc acc ctg gaa gat gcc ctg tcc aac gtg gac      48
  Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp
      -90                      -85                      -80

ctg ctt gaa gag ctt ccc ctc ccc gac cag cag cca tgc atc gag cct      96
Leu Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro
      -75                      -70                      -65

cca cct tcc tcc atc atg tac cag gct aac ttt gac aca aac ttt gag     144
Pro Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu
      -60                      -55                      -50

gac agg aat gca ttt gtc acg ggc att gca agg tac att gag cag gct     192
Asp Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala
      -45                      -40                      -35                      -30

aca gtc cac tcc agc atg aat gag atg ctg gag gaa gga cat gag tat     240
Thr Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr
      -25                      -20                      -15

gcg gtc atg ctg tac acc tgg cgc agc tgt tcc cgg gcc att ccc cag     288
Ala Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln
      -10                      -5                      1

gtg aaa tgc aac gag cag ccc aac cga gta gag atc tat gag aag aca     336
Val Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr
      5                      10                      15

gta gag gtg ctg gag ccg gag gtc acc aag ctc atg aag ttc atg tat     384
Val Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr
      20                      25                      30                      35

ttt cag cgc aag gcc atc gag cgg ttc tgc agc gag gtg aag cgg ctg     432
Phe Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu
      40                      45                      50

tgc cat gcc gag cgc agg aag gac ttt gtc tct gag gcc tac ctc ctg     480
Cys His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu
      55                      60                      65

acc ctt ggc aag ttc atc aac atg ttt gct gtc ctg gat gag cta aag     528
Thr Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys
      70                      75                      80

aac atg aag tgc agc gtc aag aat gac cac tcc gcc tac aag agg gca     576
Asn Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala
      85                      90                      95

gca cag ttc ctg cgg aag atg gca gat ccc cag tct atc cag gag tcg     624
Ala Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser
      100                      105                      110                      115

cag aac ctt tcc atg ttc ctg gcc aac cac aac agg atc acc cag tgt     672
Gln Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys
      120                      125                      130

ctc cac cag caa ctt gaa gtg atc cca ggc tat gag gag ctg ctg gct     720
Leu His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala
      135                      140                      145

gac att gtc aac atc tgt gtg gat tac tac gag aac aag atg tac ctg     768
Asp Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu
      150                      155                      160

act ccc agt gag aaa cat atg ctc ctc aag gta aaa ctc ccc     810
Thr Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
      165                      170                      175

tgaggccgca cccatggagc ctgggcttac cctctcacct tcttcttatt aaaaatccgt     870
tttaaaaaaac aaaaaaaaaaa aaa                                         893

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<210> 114

<211> 1475

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..459

<221> sig_peptide

<222> 55..120

<223> Von Heijne matrix

score 7.2

seq GLWLALVDGLVRS/SP

<221> polyA_signal

<222> 1444..1449

<221> polyA_site

<222> 1462..1475

<400> 114

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cagttccgca gctacgtgtg ggacccgctg ctgatecctgt cgcagatcgt cctc atg      57
                                     Met
cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg gcg ctg gtg gac      105
Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp
      -20                      -15                      -10
ggg cta gtg cga agc agc ccc tcg ctg gac cag atg ttc gac gcc gag      153
Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala Glu
      -5                      1                      5                      10
atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc atg atg tcc ttc      201
Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe
                      15                      20                      25
atc ttc aac gcc ctc acc tgt gcc ctg ggc ttg ctg tac ttc atc cgg      249
Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg
                      30                      35                      40
cga gga aag cag tgt ctg gat ttc act gtc act gtc cat ttc ttt cac      297
Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His
                      45                      50                      55
ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc tcg gcg ctg acc      345
Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr
      60                      65                      70                      75
tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg gct gtc atc ggg      393
Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly
                      80                      85                      90
gag tac ctg tgc atg cgg acg gag ctc aag gag ata ccc ctc aac tca      441
Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn Ser
                      95                      100                      105
gcc cct aaa tcc aat gtc tagaatcagg ccctttggac atcccgtga      489
Ala Pro Lys Ser Asn Val
      110
cacttgggcc ccttaacacc ttgggctgct cagaccctcc agatgaggtc cagcccagat      549
ctgagaggaa ccctggaaat gtgaagtctc tgttggtgtg ggagagatag tgagggcctg      609
tcaaagaagg caggtagcag tcagcatgac agctgcaaga atgacctctg tctgttgaag      669
ccttggtatc tgagaggtca ggaaggggac ctctttgagg gtaataacat aattggaacc      729
atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga gaaaaaaaaat      789
caaggatata tgattggagc aaaccacttc ttttagtcac tgtcttacct ccctgggaca      849
gctgttacct ttgcagtgtt gccgaatcac agcagttacc tttgcaatgt tgccgaatca      909
cagcagttct gttggagaaa cgcttggttt ccggatccag agccacagaa agaaatgtag      969
gtgtgaagta ttaggctgct gtcagggaga ggatggcaga tggaggcatc aagcacaagg      1029
aaaatgcaca acctgtgccc tggtatacac acgttcatgt gcgcccaga acctatgact      1089
ttcttccagt tcttcttacc aggtcccat cctgctgcca gctctcaaca tagcaggcca      1149
taggacccag agaagaatcc cagtgttgct caaagtctga ccatcataaa gacactgcct      1209
gtcttctagg aatgaccagg caccagctc ccactggact ccaatTTTTT ttctgctt      1269
atttagaatt ctttggcggg aagggtatga tgggttccca gagacaagaa gcccaacctt      1329
ctggcctggg ctgtgctgat agtgctgagg gagataggaa tttgctgcta agatttttct      1389

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ttgggggtgga gtttcctctg tgaggggctt gcagctatcc ttcctgtgta tacaaataca 1449
gtattttcca tgaaaaaaaa aaaaaa 1475

<210> 115
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 48..248

<221> sig_peptide
<222> 48..161
<223> Von Heijne matrix
score 6.3
seq LVFALVTAVCCCLA/DG

<221> polyA_signal
<222> 283..288

<221> polyA_site
<222> 308..321

<400> 115
gctgagaaga gttgagggaa agtgctgctg ctgggtctgc agacgcg atg aat aac 56
Met Asn Asn
gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc 104
Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly
-35 -30 -25 -20
cac gtg aag atg ctg cgg ctg gtg ttt gca ctt gtg aca gca gta tgc 152
His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr Ala Val Cys
-15 -10 -5
tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc 200
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro
1 5 10
aac ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg 248
Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
15 20 25
tgattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca 308
aaaaaaaaaaa aaa 321

<210> 116
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..399

<221> sig_peptide
<222> 25..186
<223> Von Heijne matrix
score 3.5
seq SILAQVLDQSARA/RL

<400> 116

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ctgctccagc gctgacgccg agcc atg gcg gac gag gag ctt gag gcg ctg      51
      Met Ala Asp Glu Glu Leu Glu Ala Leu
      -50
agg aga cag agg ctg gcc gag ctg cag gcc aaa cac ggg gat cct ggt      99
Arg Arg Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly
-45      -40      -35      -30
gat gcg gcc caa cag gaa gca aag cac agg gaa gca gaa atg aga aac      147
Asp Ala Ala Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn
      -25      -20      -15
agt atc tta gcc caa gtt ctg gat cag tcg gcc cgg gcc agg tta agt      195
Ser Ile Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser
      -10      -5      1
aac tta gca ctt gta aag cct gaa aaa act aaa gca gta gag aat tac      243
Asn Leu Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr
      5      10      15
ctt ata cag atg gca aga tat gga caa cta agt gag aag gta tca gaa      291
Leu Ile Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu
      20      25      30      35
caa ggt tta ata gaa atc ctt aaa aaa gta agc caa caa aca gaa aag      339
Gln Gly Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys
      40      45      50
aca aca aca gtg aaa ttc aac aga aga aaa gta atg gac tct gat gaa      387
Thr Thr Thr Val Lys Phe Asn Arg Arg Lys Val Met Asp Ser Asp Glu
      55      60      65
gat gac gat tat tgaactacaa gtgctcacag actagaactt aacggaacaa      439
Asp Asp Asp Tyr
      70
gtctaggaca g      450

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<210> 117
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..1137

<221> sig_peptide
 <222> 10..72
 <223> Von Heijne matrix
 score 6.5
 seq LLTLLPPPLYT/RH

<221> polyA_signal
 <222> 1144..1149

<221> polyA_site
 <222> 1162..1173

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<400> 117
gagctgctt atg gga cac cgc ttc ctg cgc ggc ctc tta acg ctg ctg ctg      51
      Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu
      -20      -15      -10
ccg ccg cca ccc ctg tat acc cgg cac cgc atg ctc ggt cca gag tcc      99
Pro Pro Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser
      -5      1      5
gtc ccg ccc cca aaa cga tcc cgc agc aaa ctc atg gca ccg ccc cga      147
Val Pro Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
      10      15      20      25

```

atc ggg acg cac aat ggc acc ttc cac tgc gac gag gca ctg gca tgc 195
 Ile Gly Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys
 30 35 40
 gca ctg ctt cgc ctc ctg ccg gag tac cgg gat gca gag att gtg cgg 243
 Ala Leu Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg
 45 50 55
 acc cgg gat ccc gaa aaa ctc gct tcc tgt gac atc gtg gtg gac gtg 291
 Thr Arg Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val
 60 65 70
 ggg ggc gag tac gac cct cgg aga cac cga tat gac cat cac cag agg 339
 Gly Gly Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg
 75 80 85
 tct ttc aca gag acc atg agc tcc ctg tcc cct ggg agg ccg tgg cag 387
 Ser Phe Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln
 90 95 100 105
 acc aag ctg agc agt gcg gga ctc atc tat ctg cac ttc ggg cac aag 435
 Thr Lys Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys
 110 115 120
 ctg ctg gcc cag ttg ctg ggc act agt gaa gag gac agc atg gtg ggc 483
 Leu Leu Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly
 125 130 135
 acc ctc tat gac aag atg tat gag aac ttt gtg gag gag gtg gat gct 531
 Thr Leu Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala
 140 145 150
 gtg gac aat ggg atc tcc cag tgg gca gag ggg gag cct cga tat gca 579
 Val Asp Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala
 155 160 165
 ctg acc act acc ctg agt gca cga gtt gct cga ctt aat cct acc tgg 627
 Leu Thr Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp
 170 175 180 185
 aac cac ccc gac caa gac act gag gca ggg ttc aag cgt gca atg gat 675
 Asn His Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp
 190 195 200
 ctg gtt caa gag gag ttt ctg cag aga tta gat ttc tac caa cac agc 723
 Leu Val Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser
 205 210 215
 tgg ctg cca gcc cgg gcc ttg gtg gaa gag gcc ctt gcc cag cga ttc 771
 Trp Leu Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe
 220 225 230
 cag gtg gac cca agt gga gag att gtg gaa ctg gcg aaa ggt gca tgt 819
 Gln Val Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys
 235 240 245
 ccc tgg aag gag cat ctc tac cac ctg gaa tct ggg ctg tcc cct cca 867
 Pro Trp Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro
 250 255 260 265
 gtg gcc atc ttc ttt gtt atc tac act gac cag gct gga cag tgg cga 915
 Val Ala Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg
 270 275 280
 ata cag tgt gtg ccc aag gag ccc cac tca ttc caa agc cgg ctg ccc 963
 Ile Gln Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro
 285 290 295
 ctg cca gag cca tgg cgg ggt ctt cgg gac gag gcc ctg gac cag gtc 1011
 Leu Pro Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val
 300 305 310
 agt ggg atc cct ggc tgc atc ttc gtc cat gca agc ggc ttc att ggc 1059
 Ser Gly Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly
 315 320 325
 ggt cac cgc acc cga gag ggt gcc ttg agc atg gcc cgt gcc acc ttg 1107
 Gly His Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu
 330 335 340 345
 gcc cag cgc tca tac ctc cca caa atc tcc tagtctaata aaaccttcca 1157
 Ala Gln Arg Ser Tyr Leu Pro Gln Ile Ser

350
tctcaaaaaa aaaaaa

355

1173

<210> 118
<211> 785
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..704

<221> sig_peptide
<222> 72..161
<223> Von Heijne matrix
score 13.2
seq LLLLSTLVIPSAA/AP

<221> polyA_signal
<222> 772..777

<400> 118
cggaatccgg gagtccggtg acccgggctg tggcttagca taaaggcggga gccagaaga 60
aggggcgggg t atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat 110
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His
-30 -25 -20
ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct 158
Leu Leu Val Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala
-15 -10 -5
gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc 206
Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu
1 5 10 15
aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa 254
Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys
20 25 30
ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac 302
Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp
35 40 45
ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag cac 350
Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His
50 55 60
cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag gta 398
Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val
65 70 75
ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg 446
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
80 85 90 95
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att 494
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
100 105 110
aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac 542
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
115 120 125
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc 590
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
130 135 140
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc 638
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
145 150 155
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc 686

Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
 160 165 170 175
 agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 734
 Arg Pro Ser Arg Gln Leu
 180
 tagcccccac cagaccctgc cccaagcacc atatggaaat aaagttcttt c 785

<210> 119
 <211> 559
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..505

<221> sig_peptide
 <222> 44..223
 <223> Von Heijne matrix
 score 4
 seq LVRRTLLVAALRA/WM

<400> 119
 agcaaccaga gggagatgat cacctgaacc actgctccaa acc atg ggc agt aaa 55
 Met Gly Ser Lys
 -60
 tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag agg cgg 103
 Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln Arg Arg
 -55 -50 -45
 cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg aag gca 151
 Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val Lys Ala
 -40 -35 -30 -25
 gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc agg acc 199
 Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg Arg Thr
 -20 -15 -10
 ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg tgg agg 247
 Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp Trp Arg
 -5 1 5
 acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg ttg agg 295
 Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu Leu Arg
 10 15 20
 gtc tac gtc atc cag gag cag gcg acg gtc aag ctc cag tcc tgc atc 343
 Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu Gln Ser Cys Ile
 25 30 35 40
 cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat gct ctc 391
 Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn Ala Leu
 45 50 55
 tgc ttg ttc cag gtc cca gag agc agc ctt gcc ttc cag act gat ggc 439
 Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe Gln Thr Asp Gly
 60 65 70
 ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag ttc cac 487
 Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu Phe His
 75 80 85
 att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg 535
 Ile Glu Ile Leu Ser Ile
 90
 cactacccta ataaatgtct gacc 559

<210> 120
 <211> 770
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..393

<221> sig_peptide
 <222> 25..150
 <223> Von Heijne matrix
 score 4.6
 seq LDPAVSLSAPAFSA

<221> polyA_signal
 <222> 734..739

<221> polyA_site
 <222> 757..770

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<400> 120
cgcagaaagg agagacacac atac atg aaa gga gga gct ttc tcc aat ctt      51
                               Met Lys Gly Gly Ala Phe Ser Asn Leu
                               -40                               -35

aat gat tcc cag ctc tca gcc tcg ttt ctg caa ccc agc ctg caa gca      99
Asn Asp Ser Gln Leu Ser Ala Ser Phe Leu Gln Pro Ser Leu Gln Ala
                               -30                               -25                               -20

aac tgt cct gct ttg gac cct gct gtg tca ctc tcc gca cca gcc ttt      147
Asn Cys Pro Ala Leu Asp Pro Ala Val Ser Leu Ser Ala Pro Ala Phe
                               -15                               -10                               -5

gcc tct gct ctt cgc tct atg aag tcc tcc cag gct gca cgg aag gac      195
Ala Ser Ala Leu Arg Ser Met Lys Ser Ser Gln Ala Ala Arg Lys Asp
   1               5               10              15

gac ttt ctc agg tct ctt agt gat gga gac tca ggg aca tca gaa cac      243
Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser Glu His
                               20               25               30

atc tca gcg gtg gtg act agc cct cgg att tcc tgc cat ggt gct gcc      291
Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly Ala Ala
                               35               40               45

att ccc acc gcc cgt gcc ctc tgc cta ggc tgt tcc tgc tgc acc gaa      339
Ile Pro Thr Ala Arg Ala Leu Cys Leu Gly Cys Ser Cys Cys Thr Glu
                               50               55               60

cgc ctc ctc ctg cca ccg ccc tcc ctc ctt tct tta gaa gcc cct gcc      387
Arg Leu Leu Leu Pro Pro Pro Ser Leu Leu Ser Leu Glu Ala Pro Ala
                               65               70               75

agc acc tgagctctct gctgattgct gttcctccca gtctgtggaa gctttgccca      443
Ser Thr
80
tatgctttcc ttaaaagggt tctgggcagg gcaggcgccc ccattttctca gggatcccct      503
ccaggacaac gccttttccct tgtgtcttca gctctcctta ccagatatct atatatttgt      563
atatattcag ttccaccaac aatgcatcaa gtactttttt ttttaagtaa agaaccgcag      623
tcatcgaaact ggagccccat tgattccctc ccctcgcct ccccaaatct ggcacctgcc      683
caaggtatcc tcagaaccat ttgggggtgc ctttggcatt ggataataga aataaaattt      743
tacctctttc tacaaaaaaa aaaaaaac      770

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<210> 121
 <211> 1213
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 58..1095

<221> sig_peptide

<222> 58..114

<223> Von Heijne matrix

score 5.4

seq LSHLLPSLRQVIQ/EP

<221> polyA_site

<222> 1202..1213

<400> 121

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cctggctttg cctttgccct gctgtgtgat cttagctccc tgcccaggcc cacagcc      57
atg gcc atg gcc cag aaa ctc agc cac ctc ctg ccg agt ctg cgg cag      105
Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln
          -15                    -10                    -5
gtc atc cag gag cct cag cta tct ctg cag cca gag cct gtc ttc acg      153
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
          1                    5                    10
gtg gat cga gct gag gtg ccg ccg ctc ttc tgg aag ccg tac atc tat      201
Val Asp Arg Ala Glu Val Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
          15                    20                    25
gcg ggc tac cgg ccg ctg cat cag acc tgg cgc ttc tat ttc cgc acg      249
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
          30                    35                    40                    45
ctg ttc cag cag cac aac gag gcc gtg aat gtc tgg acc cac ctg ctg      297
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
          50                    55                    60
gcg gcc ctg gta ctg ctg ctg cgg ctg gcc ctc ttt gtg gag acc gtg      345
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
          65                    70                    75
gac ttc tgg gga gag cca cac gcc ctg ccc ctc ttc atc att gtc ctt      393
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
          80                    85                    90
gcc tct ttc acc tac ctc tcc ctc agt gcc ttg gct cac ctc ctg cag      441
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln
          95                    100                    105
gcc aag tct gag ttc tgg cat tac agc ttc ttc ttc ctg gac tat gtg      489
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
          110                    115                    120                    125
ggg gtg gcc gtg tac cag ttt ggc agt gcc ttg gca cac ttc tac tat      537
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
          130                    135                    140
gct atc gag ccc gcc tgg cat gcc cag gtg cag gct gtt ttt ctg ccc      585
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
          145                    150                    155
atg gct gcc ttt ctc gcc tgg ctt tcc tgc att ggc tcc tgc tat aac      633
Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
          160                    165                    170
aag tac atc cag aaa cca ggc ctg ctg ggc cgc aca tgc cag gag gtg      681
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
          175                    180                    185
ccc tcc gtc ctg gcc tac gca ctg gac att agt cct gtg gtg cat cgt      729
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
          190                    195                    200                    205
atc ttc gtg tcc tcc gac ccc acc acg gat gat cca gct ctt ctc tac      777
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
          210                    215                    220
cac aag tgc cag gtg gtc ttc ttt ctg ctg gct gct gcc ttc ttc tct      825

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His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
      225                230                235
acc ttc atg ccc gag cgc tgg ttc cct ggc agc tgc cat gtc ttc ggg      873
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
      240                245                250
cag ggc cac caa ctt ttc cat atc ttc ttg gtg ctg tgc acg ctg gct      921
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
      255                260                265
cag ctg gag gct gtg gca ctg gac tat gag gcc cga cgg ccc atc tat      969
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
      270                275                280                285
gag cct ctg cac acg cac tgg cct cac aac ttt tct ggc ctc ttc ctg      1017
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
      290                295                300
ctc acg gtg ggc agc agc atc ctc act gca ttc ctc ctg agc cag ctg      1065
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
      305                310                315
gta cag cgc aaa ctt gat cag aag acc aag tgaaggggga tggcatctgg      1115
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
      320                325
tagggaggga ggtatagttg ggggacaggg gtctggggttt ggctccaagt gggaacaagg      1175
cctggtaaag ttgtttgtgt ctggccaaaa aaaaaaaaaa      1213

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<210> 122

<211> 1318

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..660

<221> sig_peptide

<222> 31..90

<223> Von Heijne matrix

score 5.4

seq AFVIACVLSLIST/IY

<221> polyA_signal

<222> 1288..1293

<221> polyA_site

<222> 1307..1318

<400> 122

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ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca      54
                        Met Asp Asn Arg Phe Ala Thr Ala
                        -20                -15
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
      -10                -5                1
gct tcc att ggc aca gac ttc tgg tat gag tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
      5                10                15                20
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
      25                30                35
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
      40                45                50

```

```

ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
      55      60      65
cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
      70      75      80
aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt      390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
      85      90      95      100
gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt      438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
      105      110      115
tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc      486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
      120      125      130
ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat      534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
      135      140      145
ccc acc att gcc acg ggc att ctc cat ctc ctt gca gtg aca aag gag      582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Val Thr Lys Glu
      150      155      160
agc atg ctt cca gct gga gct gag tcc aag cac aca gcc act cct gca      630
Ser Met Leu Pro Ala Gly Ala Glu Ser Lys His Thr Ala Thr Pro Ala
      165      170      175      180
cac gca tgc gtg caa aca ggg aag ccc aag taggagaaga ggaaagaggt      680
His Ala Cys Val Gln Thr Gly Lys Pro Lys
      185      190
tgtagggatt tgggaagaac cttgattatt ccctggagga aaagacaaat ctacttcct      740
gaaatcaccc tcgaatctac ttccaccctc agaacttaaa atgaactgca tccttttttt      800
catcttcttt tcttctccag tgaatatgat ctccaaaccc ttattttttc ttggaactgt      860
aaaatttcca ctcatggacg atgcaaccaa cagatgcaat ctctgagaag atgaaaattg      920
ggacctctta ttataaaatt gacctagctg gactcaggaa accaggggaag aagtcaatgc      980
aggcatttaa aatgtaaagt tttttctggt taaatctatt tatttttctt gtaggttgag      1040
tatttcttcc cagtttttct gctctggtgt ataacaaaca ggtcaaaatt tcccatcttt      1100
cctcctgata gtagttgaat cctaccttgc atacttaatg catagtgaag tggcatctag      1160
cagaaataca caccaccaaa acacaccacc atttcattag gtgccccaaa aattctgtat      1220
ttagcttatt tatttattgt tatttttgct ttttcttaac ccactatata ttgactgcaa      1280
acgaattaat aaattatccc ttctggaaaa aaaaaaaaaa      1318

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<210> 123

<211> 853

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..582

<221> sig_peptide

<222> 31..90

<223> Von Heijne matrix

score 5.4

seq AFVIACVLSLIST/IY

<221> polyA_signal

<222> 816..821

<221> polyA_site

<222> 840..853

<400> 123

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ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca      54
                                Met Asp Asn Arg Phe Ala Thr Ala
                                -20                                -15

ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
                                -10                                -5                                1

gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
5                                10                                15                                20

gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
                                25                                30                                35

gat gaa gca gat gaa aag act tat aat gat gca cct ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Pro Phe Arg Tyr Asn
                                40                                45                                50

ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
55                                60                                65

cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
70                                75                                80

aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt      390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
85                                90                                95                                100

gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt      438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
105                                110                                115

tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc      486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
120                                125                                130

ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat      534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
135                                140                                145

ccc acc att gcc acg ggc att ctc cat ctc ctt gca gat acc atg ctg      582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Asp Thr Met Leu
150                                155                                160

tgaagtccag gccacatgga ggtgtcctgt gtagatgctc cagctgaaat cccaagctaa      642
gctcccaact gacagccaac atcatttcca gccatgtgtg ggagccatcc tggatgtcca      702
gccttaacaa gccttcagag gacttcagcc acagctatta tcttactaca tccttgtgag      762
actctaataa agaaccaact agctgagccc aatcaacctt tggaactgat agaaataaaaa      822
tgaattgttg ttttgcgaaa aaaaaaaaaa a      853

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<210> 124

<211> 826

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..695

<221> sig_peptide

<222> 15..80

<223> Von Heijne matrix

score 8.5

seq AALLLGLMMVVTG/DE

<221> polyA_signal

<222> 795..800

<221> polyA_site

<222> 814..826

<400> 124

```

aaccagaggt gccc atg ggt tgg aca atg agg ctg gtc aca gca gca ctg      50
                Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu
                -20                                -15

tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc      98
Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
-10                                -5                                1                                5

ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag      146
Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
                10                                15                                20

ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt      194
Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
                25                                30                                35

gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag      242
Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
                40                                45                                50

ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg      290
Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
55                                60                                65                                70

gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga      338
Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
                75                                80                                85

ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag      386
Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
                90                                95                                100

aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc      434
Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
105                                110                                115

cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt      482
Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
120                                125                                130

cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga      530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
135                                140                                145                                150

ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa      578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
155                                160                                165

cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca      626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
170                                175                                180

acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
185                                190                                195

cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt      725
Gln Ala Glu Ile Ala Ala Cys
200                                205

ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccct      785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a
200                                205

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<210> 125

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..295

<221> sig_peptide

<222> 74..196

<223> Von Heijne matrix

score 5.4

seq RLLYIGFLGYCSG/LI

<221> polyA_signal

<222> 545..550

<221> polyA_site

<222> 561..571

<400> 125

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cgggtagtggt tcgtcgtggt tttccttgta gtctgtggtc tgagaccagg cctcaagtgg      60
aaacggcgctc acc atg atc gca cgg cgg aac cca gta ccc tta cgg ttt      109
                Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe
                -40                -35                -30
ctg ccg gat gag gcc cgg agc ctg ccc ccg ccc aag ctg acc gac ccg      157
Leu Pro Asp Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro
                -25                -20                -15
cgg ctc ctc tac atc ggc ttc ttg ggc tac tgc tcc ggc ctg att gat      205
Arg Leu Leu Tyr Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp
                -10                -5                1
aac ctg atc cgg cgg agg ccg atc gcg acg gct ggt ttg cat cgc cag      253
Asn Leu Ile Arg Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln
                5                10                15
ctt cta tat att acg gcc ttt ttt ttg ctg gat att atc ttg      295
Leu Leu Tyr Ile Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
20                25                30
taaaacgtga agactacctg tatgctgtga gggaccgtga aatgttttga tatatgaaat      355
tacatccaga ggattttcct gaagaagata agaaaacata tgggtgaaatt tttgaaaaat      415
tccatccaat acgttgaagt cttcaaaatg cttgctccag tttcactgat acctgctggt      475
cctgaatttg atggaacatg tttcttatga cagtgaagc ttatgctaatt ctgtatgttg      535
acaccttgta attaaaatac gtacaaaaaa aaaaaa      571

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<210> 126

<211> 659

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 440..658

<221> polyA_signal

<222> 601..606

<400> 126

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cgccttacga gctgggaggt ggtgcctctc acccagctaa ttgctctcta gcccttgccc      60
ttcacagggtg ttggtgcctg ccgtgaacgc attctgacct gggccgtatc tgtctcccaa      120
gactttgtgc ctatggttgg ggacagagtg aggtcggtgc cttgacgacg acagcatgcg      180
gcccgtagtc ctccaaagtg tgagcttgcg gcggaccgag gccacactgc ctccctgcct      240
gtcttcgcca ggactcgtga ctgcgtccgc agaagaaatc acaacagcgc tggaattgct      300
agtttgctag gcagcatctt ttggacctgc gaaccatatg catttcacct caaatctggt      360
tccaagttga aaacctttgg gtctttctat gcgaacggat tgaagaaacg caaaaagttt      420
ctacggactt taaattaaa atg gaa aaa tat gaa aac ctg ggt ttg gtt gga      472
                Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly
                1                5                10

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gaa ggg agt tat gga atg gtg atg aag tgt agg aat aaa gat act gga      520
Glu Gly Ser Tyr Gly Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly
      15                20                25
aga att gtg gcc ata aag aag ttc tta gaa agt gac gat gac aaa atg      568
Arg Ile Val Ala Ile Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met
      30                35                40
gtt aaa aag att gca atg cga gaa gtc aag tta cta aag caa ctt agg      616
Val Lys Lys Ile Ala Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg
      45                50                55
cat gaa aac ttg gtg aat ctc ttg gaa gtg tgt aaa aaa aaa a      659
His Glu Asn Leu Val Asn Leu Leu Glu Val Cys Lys Lys Lys
      60                65                70

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<210> 127
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..283

<221> sig_peptide
 <222> 38..85
 <223> Von Heijne matrix
 score 4.1
 seq LLPATSLAGPVLS/TL

<221> polyA_signal
 <222> 257..262

```

<400> 127
cacctgaatc ccaggaaccc tcaatgaggt cttcaag atg aag aga ctg ctg cca      55
                        Met Lys Arg Leu Leu Pro
                        -15
gct acc agc ctg gct ggc cct gtc ctg tcc acc ctc att gcc cca act      103
Ala Thr Ser Leu Ala Gly Pro Val Leu Ser Thr Leu Ile Ala Pro Thr
-10                -5                1                5
ccc atg ttg ttt tgt gaa gat aaa agc tgg gat ctt ttt ctt ttt ttt      151
Pro Met Leu Phe Cys Glu Asp Lys Ser Trp Asp Leu Phe Leu Phe Phe
      10                15                20
aag tct cac aag aca tgg ggc atc tcc aca aat tta agt tcc tgt cca      199
Lys Ser His Lys Thr Trp Gly Ile Ser Thr Asn Leu Ser Ser Cys Pro
      25                30                35
ttt gga aat ttg ttt cta tgt gta cag ttt gtc aga gaa aaa caa agt      247
Phe Gly Asn Leu Phe Leu Cys Val Gln Phe Val Arg Glu Lys Gln Ser
      40                45                50
ttt tgt atg aat aca gaa tgt gat tta cgc aag aat tgacaaaaaa      293
Phe Cys Met Asn Thr Glu Cys Asp Leu Arg Lys Asn
      55                60                65
aaaaaaaaa

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<210> 128
 <211> 477
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 121..477

<221> sig_peptide
 <222> 121..288
 <223> Von Heijne matrix
 score 3.5
 seq SSCADSFVSSSSS/QP

<400> 128
 cctcggagca ggcggagtaa agggacttga gcgagccagt tgccggatta ttctatttcc 60
 cctccctctc tcccgccccg tatctctttt cacccttctc ccaccctcgc tcgcgtagcc 120
 atg gcg gag ccg tcg gcg gcc act cag tcc cat tcc atc tcc tcg tcg 168
 Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
 -55 -50 -45
 tcc ttc gga gcc gag ccg tcc gcg ccc ggc ggc ggc ggc agc cca gga 216
 Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
 -40 -35 -30 -25
 gcc tgc ccc gcc ctg ggg acg aag agc tgc agc tcc tcc tgt gcg gat 264
 Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
 -20 -15 -10
 tcc ttt gtt tct tcc tct tcc tct cag cct gta tct cta ttt tcg acc 312
 Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
 -5 1 5
 tca caa gag gga ttg agc tct ctt tgc tct gat gag cca tct tca gaa 360
 Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
 10 15 20
 att atg act tct tcc ttt ctt tca tct tct gaa ata cat aac act ggc 408
 Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
 25 30 35 40
 ctt aca ata cta cat gga gaa aaa agc cat gtg tta ggc agc cag cct 456
 Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
 45 50 55
 att tta gcc aaa aaa aaa aaa 477
 Ile Leu Ala Lys Lys Lys
 60

<210> 129
 <211> 323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..163

<221> polyA_signal
 <222> 292..297

<221> polyA_site
 <222> 310..323

<400> 129
 a gct ttc gtg tgg gag cca gct atg gtg cgg atc aat gcg ctg aca gca 49
 Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
 1 5 10 15
 gcc tct gag gct gcg tgc ctg atc gtg tct gta gat gaa acc atc aag 97
 Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
 20 25 30
 aac ccc cgc tcg act gtg gat gct ccc aca gca gca ggc cgg ggc cgt 145

Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
 35 40 45
 ggt cgt ggc cgc ccc cac tgagaggcac cccacccatc acatggctgg 193
 Gly Arg Gly Arg Pro His
 50
 ctggctgctg ggtgcactta ccctccttgg cttggttact tcattttaca aggaaggggt 253
 agtaattggc ccactctctt cttactggag gctattttaa taaaatgtaa gacttcaaaa 313
 aaaaaaaaaa 323

<210> 130
 <211> 1392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..675

<221> sig_peptide
 <222> 46..87
 <223> Von Heijne matrix
 score 5.3
 seq LTLGLSFILAGL/IV

<221> polyA_signal
 <222> 1364..1369

<221> polyA_site
 <222> 1383..1392

<400> 130
 ctccgagttg ccaccagga aaaagagggc tcctctggga gatgt atg ctt act ctc 57
 Met Leu Thr Leu
 tta ggc ctt tca ttc atc ttg gca gga ctt att gtt ggt gga gcc tgc 105
 Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
 -10 -5 1 5
 att tac aag tac ttc atg ccc aag agc acc att tac cgt gga gag atg 153
 Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
 10 15 20
 tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag 201
 Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
 25 30 35
 cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac 249
 Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
 40 45 50
 aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac 297
 Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
 55 60 65 70
 cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg 345
 Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
 75 80 85
 gac ttg ttg ctg ggg atc tgc tat ctg atg ccc ctc aat act tct att 393
 Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
 90 95 100
 gtt atg cct cca aaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt 441
 Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
 105 110 115
 ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct 489
 Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu Asp Leu Val Ala
 120 125 130

```

gtg gag gaa att cgt gat gtt agt aac ctt ggc atc ttt att tac caa      537
Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile Phe Ile Tyr Gln
135              140              145              150
ctt tgc aat aac aga aag tcc ttc cgc ctt cgt cgc aga gac ctc ttg      585
Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg Arg Asp Leu Leu
              155              160              165
ctg ggt ttc aac aaa cgt gcc att gat aaa tgc tgg aag att aga cac      633
Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp Lys Ile Arg His
              170              175              180
ttc ccc aac gaa ttt att gtt gag acc aag atc tgt caa gag              675
Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys Gln Glu
              185              190              195
taagaggcaa cagatagagt gtccttggtg ataagaagtc agagatttac aatatgactt      735
taacattaag gtttatggga tactcaagat atttactcat gcatttactc tattgcttat      795
gctttaaaaa aaggaaaaaa aaaaaactac taaccactgc aagctcttgt caaatTTtag      855
ttaattggc attgcttggt ttttgaaact gaaattacat gagtttcatt ttttctttgc      915
atttataggg tttagatttc tgaaagcagc atgaatatat cacctaacat cctgacaata      975
aattccatcc gttgtttttt ttgtttgttt gttttttctt ttcctttaag taagctcttt      1035
attcatctta tgggtggagca attttaaaat ttgaaatatt ttaaattggt tttgaacttt      1095
ttgtgtaaaa tatatcagat ctcaacattg ttggtttctt ttgtttttca ttttgtacaa      1155
ctttcttgaa tttagaaatt acatctttgc agttctgtta ggtgctctgt aattaacctg      1215
acttatatgt gaacaatttt catgagacag tcatttttaa ctaatgcagt gattctttct      1275
cactactatc tgtattgtgg aatgcacaaa attgtgtagg tgctgaatgc tgtaaggagt      1335
ttaggttgta tgaattctac aaccctataa taaattttac tctatacaaa aaaaaaa      1392

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<210> 131

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 62..385

<221> polyA_signal

<222> 974..979

<221> polyA_site

<222> 987..999

<400> 131

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cctgaatgac ttgaatgttt ccccgccctga gctaacagtc catgtgggtg attcagctct      60
g atg gga tgt gtt ttc cag agc aca gaa gac aaa tgt ata ttc aag ata      109
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1              5              10              15
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta      157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
              20              25              30
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc      205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
              35              40              45
gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc      253
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
              50              55              60
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc      301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
              65              70              75              80
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg      349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
              85              90              95

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```

ctt cca gag gag ccc aaa ggt acg caa atg ctt act taaagagggg      395
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
      100                      105
ccaaggggca agagctttca tgtgcaagag gcaaggaaac tgattatctt gagtaaattgc      455
cagccttttg gctaagtact taccacagag tgaatcttca aaaaatgatc ataattattt      515
cagtcaataa aaatagaggt attttattaa ataaaatatt gataattatt gtattattac      575
tttaaacaca cttccccctc acaaaaagccc tgtgaaggat gttttgttca catatatgtc      635
caaatatgtt ttggacacat atttattaaa tggaataaat agtacttgaa ccctggcacc      695
tctgacaaca aagtccatgt tctttttact atgccctaac acctttcatc agttatccac      755
attgatgcta catctgtatt ttataggtac cctatgttag gtgttctggg ggatagaaaa      815
gaaataagca ggccaggctc agtgggtcat gcctgtaatc cttagcatttt gggaggctga      875
ggcagcagaa ctgcctgagc cccagggttc aagactgcag tgagctatga tggcaccact      935
gcattctagc ctgggtgaca gagcaagact ctgtctaaaa taaaaaaga gaaaaaaaaa      995
aaaa

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<210> 132
 <211> 725
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 422..550

<221> sig_peptide
 <222> 422..475
 <223> Von Heijne matrix
 score 4.5
 seq LRWLMPVIPALWG/AE

<221> polyA_site
 <222> 714..725

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<400> 132
tctgcgaggg tgggagagaa aattaggggg agaaaggaca gagagagcaa ctaccatcca      60
tagccagata ggtgagtaaa tatatttgca gtaacctatt tgctattcct tgctgcaact      120
gtgtttaatg ttccttccag aatcagagag agtattgccca tccaagaaat cgtttttaga      180
tatgacattt gagctatcat cttgagacca atacctaaaa caatttcagt ttaagaaatg      240
tctaggtatg gtgaaaacac agtttaaaac cagcaaaaca gaattttattg ccctcagcga      300
atacccacaa tgtacatata ctttgtatct ctgaaagcaa agcaagcatg ccaagtagtt      360
tttatttacc tgtacctata atacagcaag gtgaaacagg atatattttt gaagtttaaa      420
a atg tct tca ggc cgg ctg cgg tgg ctc atg cct gta atc cca gca ctt      469
  Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
      -15                      -10                      -5
tgg gga gcc gag aag ggt gaa tca cct gag gtc agc agt ttt gag acc      517
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
      1                      5                      10
agg ctg gcc aac atg gcg aaa ccc tgt ctc tac tgaaaataca aaaattagct      570
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
      15                      20                      25
gggtgtggtg gcgggcgcct gtagtcccag ctacttggga gactgaggca ggagaattgc      630
ttgaacacgg aaggcggaag ttgcagtaag ctgagatcgt gccaccgcac accagcttgg      690
gcaacagagt gagactccct ctcaaaaaaa aaaaa
      725

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<210> 133
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 124..231

<221> polyA_site

<222> 387..400

<400> 133

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ctcgctctc ctggcttctg gtatgcacca gcaattcctg gcgttccttg gtccttagaa      60
gcacactcc tatcacatgg tcattctcac cctgtgtgac ttcacactac cttttctctg      120
tgc atg tct gcc cga atc cct ttt tat aag gac acc agt cag att aga      168
    Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg
      1             5             10             15
tta ggg tct acc ata ata cct cat ttt aac tta atc acc ttt gta aag      216
Leu Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys
      20             25             30
acc ttt ttc caa ata tagtcaact ctgaggtact gatggtagg atctcaacat      271
Thr Phe Phe Gln Ile
      35
accttttttg ggaggacaca attgaaccca taacagggtg tttgcaagga agagttaaaa      331
tttgaaagaa aggtggtatt tgcttagata gatagggcac agctttctag gtgacaaaaa      391
aaaaaaaaa                                         400

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<210> 134

<211> 1053

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 131..1051

<221> sig_peptide

<222> 131..169

<223> Von Heijne matrix

score 4.2

seq MLAVSLTVPLLGA/MM

<221> polyA_signal

<222> 1019..1024

<400> 134

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gagcgaggcg gacgggctgc gacagcgccg gcccctgcgg ccgcaggctg tcacagacga      60
tgatggccag gcccgggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt      120
gacottcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc      169
    Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
      -10             -5
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa      217
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
      1             5             10             15
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga      265
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
      20             25             30
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata      313
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
      35             40             45
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc      361
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val
      50             55             60

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gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg      409
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser
65                               70                               75                               80
ggc cct tgc aaa acc cga gat gat gag cct gtg tgt ggg aga ccc ctg      457
Gly Pro Cys Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu
85                               90                               95
ggg atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tgc      505
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys
100                            105                            110
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg      553
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu
115                            120                            125
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat      601
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn
130                            135                            140
gat ctt aca gtc tct cag gat ggg agg aag att tat ttc acc gat tct      649
Asp Leu Thr Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser
145                            150                            155                            160
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc      697
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly
165                            170                            175
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta      745
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val
180                            185                            190
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct      793
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser
195                            200                            205
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata      841
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile
210                            215                            220
cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt      889
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe
225                            230                            235                            240
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct      937
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser
245                            250                            255
ggg ggg tac tgg gtg ggc atg tcg acc atc cgc cct aac cct ggg ttt      985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
260                            265                            270
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att      1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
275                            280                            285
ttt aag gca aaa aaa aaa aa      1053
Phe Lys Ala Lys Lys Lys
290

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<210> 135

<211> 1128

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 86..403

<221> sig_peptide

<222> 86..181

<223> Von Heijne matrix

score 8.8

seq VPMLLLIVGGSFG/LR

<221> polyA_signal

<222> 1097..1102

<221> polyA_site

<222> 1117..1128

<400> 135

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cgtcttggtg agagcgtgag ctgctgagat ttgggagttc gcgctaggcc cgcttgaggat      60
tctgagccga tggaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct      112
                               Met Phe Ala Pro Ala Val Met Arg Ala
                               -30                               -25

ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg      160
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu
                               -20                               -15                               -10

att gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat      208
Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr
                               -5                               1                               5

gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa      256
Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys
10                               15                               20                               25

gag aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc      304
Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser
                               30                               35                               40

aag ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat      352
Lys Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp
                               45                               50                               55

cct gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca      400
Pro Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr
60                               65                               70

act tgactctgct gattcttttt tccnnntttt ttttttttta aataaaaata      453
Thr

ctattaactg gacttcctaa tatatacttc tatcaagtgg aaaggaaatt ccaggcccat      513
ggaaacttgg atatgggtaa ttgatgaca aataatcttc actaaagggtc atgtacaggt      573
ttttatactt cccagctatt ccatctgtgg atgaaagtaa caatgttggc cacgtatatt      633
ttacacctcg aaataaaaaa tgtgaatact gtcctaaaaa aaaaaaccag taccgtgtag      693
tctctctcgt ggcttggtatt tacactgggc aacgtggttg gaatgtatct ggctcagaac      753
tatgatatac caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag      813
aagaaacccc ctagtgcctg agactgcctc cagcactgcc ttcaggatat accgattcta      873
ctgctcttga gggcctcggt tactatctga accaaaagct tttgttttcg tctccagcct      933
cagcacttct cttcttttgc agaccctgtg ttttttgcct taaagcaagc aaaatggggc      993
cccaatttga gaactaccgc acgtttccaa catactcacc tcttcccata atccctttcc      1053
aactgcatgg gaggttctaa gactggaatt atggtgctag attagtaaac atgactttta      1113
acgaaaaaaaa aaaaaa                                     1128

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<210> 136

<211> 254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 37..162

<221> sig_peptide

<222> 37..93

<223> Von Heijne matrix

score 9.5

seq LMCLSLCTAFALS/KP

<221> polyA_signal

<222> 224..229

<221> polyA_site

<222> 243..254

<400> 136

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tgtgctgtgg gggctacgag gaaagatcta attatc atg gac ctg cga cag ttt      54
                                   Met Asp Leu Arg Gln Phe
                                   -15
ctt atg tgc ctg tcc ctg tgc aca gcc ttt gcc ttg agc aaa ccc aca      102
Leu Met Cys Leu Ser Leu Cys Thr Ala Phe Ala Leu Ser Lys Pro Thr
      -10      -5      1
gaa aag aag gac cgt gta cat cat gag cct cag ctc agt gac aag gtt      150
Glu Lys Lys Asp Arg Val His His Glu Pro Gln Leu Ser Asp Lys Val
      5      10      15
cac aat gat att tgatagaacc aattgttgta cataaaacag atctgcgcat      202
His Asn Asp Ile
20
atatatatat gtataaaaaa taataaaata atggaagatg aaaaaaaaaa aa      254

```

<210> 137

<211> 886

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..381

<221> sig_peptide

<222> 31..90

<223> Von Heijne matrix

score 5.4

seq AFVIACVLSLIST/IY

<221> polyA_site

<222> 875..886

<400> 137

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ggaggatggg cgagcagtct gaatggcaga atg gat aac cgt ttt gct aca gca      54
                                   Met Asp Asn Arg Phe Ala Thr Ala
                                   -20      -15
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
      -10      -5      1
gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
      5      10      15      20
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
      25      30      35
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
      40      45      50
ggc aca gtg gga ttg tgg gga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Gly Arg Cys Ile Thr Ile Pro Lys Asn Met
      55      60      65
cat tgg tat agc cca cca gaa agg aca ggt att tct ctt att tta act      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Gly Ile Ser Leu Ile Leu Thr

```

70	75	80	
tct gtc ttc ttc acc tgg tta ata ata gac aaa acg acg taatgattgc			391
Ser Val Phe Phe Thr Trp Leu Ile Ile Asp Lys Thr Thr			
85	90	95	
ccaattacat gtaagcaggt ttgttggttc tctctctcct taaagaaata aatcgtgtat			451
cttctctttc tactgccttc tctccccaac ttctttgcat taccatggta ctcatcaata			511
ttggttggtat gaggaacttt tcttatcttg ggaaagcctt aatggctttt ttttttctta			571
tttactcact cattaataata cttttcatta ctctaacaca tgttataaag aaatagttgg			631
aaaagtgcac cgaaagactt ttaaaaatat ttggtaacta gtaaaaggac taccatcgaa			691
aatcaactca aaaaattgtc cttttatggg ttagctgtat tataatacat atctatcatt			751
tgccctgtg tcttagagga tataatttga ccagctctac atttaatctg tgtaattatg			811
agactgtttt acaacaatct tgatgcagag ttggtaggtt aagaaatttg tattacagaa			871
gttaaaaaaa aaaaa			886

<210> 138

<211> 1244

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..579

<221> sig_peptide

<222> 46..156

<223> Von Heijne matrix

score 3.5

seq LVFNFLILILT/IW

<400> 138

cccttatcca gggtnttatc tanggaatcc cnnnaagact gggga atg gag aga cag	57
Met Glu Arg Gln	
-35	
tca agg gtt atg tca gaa aag gat gag tat cag ttt caa cat can nna	105
Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe Gln His Xaa Xaa	
-30 -25 -20	
gcg gng gan ctg ctt gtc ttc aat ttt ttg ctc atc ctt acc att ttg	153
Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile Leu Thr Ile Leu	
-15 -10 -5	
aca atc tgg tta ttt aaa aat cat cga ttc cgc ttc ttg cat gaa act	201
Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe Leu His Glu Thr	
1 5 10 15	
gga gga gca atg gtg tat ggc ctt ata atg gga cta att tca cga tat	249
Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu Ile Ser Arg Tyr	
20 25 30	
gct aca gca cca act gat att gaa agt gga act gtc tgt gac tgt gta	297
Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val Cys Asp Cys Val	
35 40 45	
aaa cta act ttc agt cca cca act ctg ctg gtt aat gtc act gac caa	345
Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn Val Thr Asp Gln	
50 55 60	
gtt tat gaa tat aaa tac aaa aga gaa ata agt cag cac aac atc aat	393
Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln His Asn Ile Asn	
65 70 75	
cct cat caa gga aat gct ata ctt gaa aag atg aca ttt gat cca gaa	441
Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr Phe Asp Pro Glu	
80 85 90 95	
atc ttc ttc aat gtt tta ctg cca cca att ata ttt cat gca gga tat	489
Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe His Ala Gly Tyr	
100 105 110	

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agt cta aag aag aga cac ttt ttt caa aac tta gga tct att tta acg      537
Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly Ser Ile Leu Thr
      115                      120                      125
tat gcc ttc ttg gga act gcc atc tcc tgc atc gtc ata ggg      579
Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val Ile Gly
      130                      135                      140
taagtgcacat tccgagctca agttgcaggt ggctgtgggg tctgtgatct gtgtgagga      639
tctaacactt ccaggattct tgctggctgg gaaaattgtc ttttttttag tatatcacat      699
atttgatgt tttttctgac ttaattccac ggcttctgac aaatacaagg cttcaaata      759
aagcaaaacta gaggattgct ggactttctc tgtgagttct ggacttctga cttaggaat      819
gtggatcact tgccttgagt tatgtgaagc gcattgcatt cttcttttag tttgagtaat      879
gccgatatgg tcaactgcatt cttttttgtc ttgtattgag agaccttacc tgtatttggc      939
aggagtgcaa aagtaactat atgccaagag ttttctttct aaaggaaagt ttacaagaca      999
gcagtctgaa acagatatgn tccaaatatn naacagagtt gcttaataca gggatagctt     1059
ttcagttaat accctgtaga atgcagactc tttntttcat tgtattttct tgattatgct     1119
actgagccct aagtcacacg ttatatactc tggcttgcag ctcatacataa agtaaaatgt     1179
ggtaccaaata ggtgaaggca atccagcctn tgataatccc gtccaataca ttaaagntcc     1239
actgc                                           1244

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<210> 139
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..469

<221> sig_peptide
 <222> 92..172
 <223> Von Heijne matrix
 score 7.9
 seq VVVLALGFLGCGY/AK

<221> polyA_signal
 <222> 454..459

<221> polyA_site
 <222> 458..471

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<400> 139
gcaagtgcag aagtcgggtga cgggtgggcat ctgggtgtca atcgatgggg catcctttct      60
gaagatcttc gggccactgt cgtccagtgc c atg cag ttt gtc aac gtg ggc      112
                                Met Gln Phe Val Asn Val Gly
                                -25
tac ttc ctc atc gca gcc ggc gtt gtg gtc ctt gct ctt ggt ttc ctg      160
Tyr Phe Leu Ile Ala Ala Gly Val Val Val Leu Ala Leu Gly Phe Leu
-20                      -15                      -10                      -5
ggc tgc tat ggt gct aag act gag agc atg tgt gcc ctc gtg acg ttc      208
Gly Cys Tyr Gly Ala Lys Thr Glu Ser Met Cys Ala Leu Val Thr Phe
      1                      5                      10
ttc ttc atc ctc ctc ctc atc ttc att gct gag gtt gca gct gct gtg      256
Phe Phe Ile Leu Leu Leu Ile Phe Ile Ala Glu Val Ala Ala Ala Val
      15                      20                      25
gtc gcc ctg gtg tac acc aca atg gct gag cac ttc ctg acg ttg ctg      304
Val Ala Leu Val Tyr Thr Met Ala Glu His Phe Leu Thr Leu Leu
      30                      35                      40
gta gtg cct gcc atc aag aaa gat tat ggt tcc cag gaa gac ttc act      352
Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp Phe Thr
45                      50                      55                      60

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caa gtg tgg aac acc acc atg aaa ggg ctc aag tgc cgt ggc ttc acc      400
Gln Val Trp Asn Thr Thr Met Lys Gly Leu Lys Cys Arg Gly Phe Thr
      65                                70                                75
aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg cat aaa cct      448
Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met His Lys Pro
      80                                85                                90
gtt aca atg aaa aaa aaa aa      471
Val Thr Met Lys Lys Lys Lys
      95

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<210> 140
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..675

<221> sig_peptide
 <222> 154..498
 <223> Von Heijne matrix
 score 4.8
 seq PLRLLNLLILIEG/GV

<221> polyA_signal
 <222> 819..824

<221> polyA_site
 <222> 838..849

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<400> 140
cccctatctc cagacctcat tcgcaatgaa gtagaatgtc tgaaagcaga tttcaaccac      60
agaatcaagg aggttctctt caactccctc ttcagtgcct actatgttgc atttctcccc      120
ctgtgttttg tgaagagtac ccagtactat gac atg cgc tgg tca tgt gag cac      174
                                Met Arg Trp Ser Cys Glu His
                                -115                                -110
ctc gtt atg gtg tgg atc aat gct ttt gtc atg ctc acc acg caa ctg      222
Leu Val Met Val Trp Ile Asn Ala Phe Val Met Leu Thr Thr Gln Leu
      -105                                -100                                -95
ttg cca tcc aaa tac tgt gat ttg cta cat aaa tca gct gct cac ctg      270
Leu Pro Ser Lys Tyr Cys Asp Leu Leu His Lys Ser Ala Ala His Leu
      -90                                -85                                -80
ggc aag tgg cag aag ttg gaa cat ggg tcc tac agc aat gct cca cag      318
Gly Lys Trp Gln Lys Leu Glu His Gly Ser Tyr Ser Asn Ala Pro Gln
      -75                                -70                                -65
cac att tgg tca gaa aat aca ata tgg cct caa ggg gtg ctg gtg cgg      366
His Ile Trp Ser Glu Asn Thr Ile Trp Pro Gln Gly Val Leu Val Arg
      -60                                -55                                -50                                -45
cac agc aga tgt tta tat aga gcc atg ggg cct tac aac gtg gca gtg      414
His Ser Arg Cys Leu Tyr Arg Ala Met Gly Pro Tyr Asn Val Ala Val
      -40                                -35                                -30
cct tca gat gta tct cat gcc cgc ttt tat ttc tta ttt cat cga cca      462
Pro Ser Asp Val Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro
      -25                                -20                                -15
tta agg ctg tta aat ctg ctc atc ctt att gag ggc ggt gtc gtc ttc      510
Leu Arg Leu Leu Asn Leu Leu Ile Leu Ile Glu Gly Gly Val Val Phe
      -10                                -5                                1
tat cag ctc tat tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt      558
Tyr Gln Leu Tyr Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu

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5           10           15           20
tcc atg gct ctc atc ttc tgc aac tac tat gtt tta ttt aaa ctt      606
Ser Met Ala Leu Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu
           25           30           35
ctc cgg gac aga ata gta tta ggc agg gca tac tcc tac cca ctc aac      654
Leu Arg Asp Arg Ile Val Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn
           40           45           50
agt tat gaa ctc aag gca aac taagctgcct ctcaacaatg agggagaact      705
Ser Tyr Glu Leu Lys Ala Asn
           55
cagataaaaaa tattttcata cgttctatatt ttttcttggtg atttttataa atatttaaga      765
tggttttatat tttgtataact attatgtttt gaaagtcggg aagagtaagg gatattaaat      825
gtatccgtaa acaaaaaaaaa aaaa      849

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<210> 141
 <211> 155
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

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<400> 141
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
   -30           -25           -20
Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
  -15           -10           -5           1
Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His Ala Val
           5           10           15
Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
           20           25           30
Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
           35           40           45
Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
           50           55           60           65
Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
           70           75           80
Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
           85           90           95
Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu Phe Leu
           100           105           110
Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
           115           120

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<210> 142
 <211> 55
 <212> PRT
 <213> Homo sapiens

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<400> 142
Met Ala Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg
1           5           10           15
Met Tyr Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe
           20           25           30
Phe Met Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln
           35           40           45
Lys Gln Lys Lys Arg Ser Asn

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50

55

<210> 143
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 143
 Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
 -20 -15 -10 -5
 Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
 1 5 10
 Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
 15 20 25
 Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
 30 35 40
 Gly Arg Lys
 45

<210> 144
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 144
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys Gln Ser
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala

175

<210> 145
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 145
 Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
 -25 -20 -15 -10
 Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5
 Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20
 Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Lys Xaa
 25 30 35
 Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn Leu Ser Phe
 40 45 50 55
 Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg Lys Asn Trp
 60 65 70
 Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu Gly Thr Tyr
 75 80 85
 Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln Ser Gln Ser
 90 95 100
 Lys Gln Lys Ser Ile Glu Glu
 105 110

<210> 146
 <211> 255
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -70...-1

<400> 146
 Met Gln Gln Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe
 -70 -65 -60 -55
 Pro Gln Ile Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val
 -50 -45 -40
 Ile Ala Asn Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn
 -35 -30 -25
 Val Val Ser Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu
 -20 -15 -10
 Ala Pro Phe Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val
 -5 1 5 10
 Gly Leu Gly Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val
 15 20 25
 Glu Asn Thr Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr
 30 35 40
 Ala Thr Ser Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp
 45 50 55
 Ile Thr Pro Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr

60		65		70	
Lys Met Ile Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr					
75		80		85	90
Val Gly Arg Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val					
	95		100		105
Glu Thr Leu Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val					
	110		115		120
Ala Arg Asn Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp					
	125		130		135
Val Val Asn Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Glu Lys					
	140		145		150
Ser Glu Ser Ala Glu Leu Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu					
155		160		165	170
Asn Leu Asn Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly					
	175		180		185

<210> 147
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<400> 147	
Met Pro Gly Thr Glu Val Leu Glu Gly Ala Thr Asp Gly Leu Ala Ala	
	-45 -40 -35
Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu Gly Gly Ser Val Ile Ser	
	-30 -25 -20
Met Ile Val Leu Leu Ile Cys Val Val Cys Leu Tyr Ile Val Cys Arg	
	-15 -10 -5
Cys Gly Ser His Leu Trp Arg Glu Ser His His	
1 5 10	

<210> 148
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 148	
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln Leu	
1 5 10 15	
Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly Asp Gly	
	20 25 30
Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln Leu Ser Ala	
	35 40 45
Thr Lys Ser Asp Asp Thr Val Val Ala Ile Pro Tyr Gly Ser Arg His	
	50 55 60
Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu Tyr Leu Glu Thr Lys	
65 70 75 80	
Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser Leu Ser Ser Thr Gly Thr	
	85 90 95
Phe Leu Val Asp Asn Ser Ser Val Asp Phe Gln Lys Phe Pro Asp Lys	
	100 105 110
Glu Ile Leu Arg Met Ala Gly Pro Leu Thr Ala Asp Phe Ile Val Lys	
	115 120 125
Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr	

130 135 140
 Gln Pro Ile Ile His Arg Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser
 145 150 155 160
 Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp
 165 170 175
 Leu Arg Ser Asn
 180

<210> 149
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 149
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 -20 -15 -10
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 -5 1 5
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 10 15 20 25
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 30 35 40
 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 45 50 55
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 60 65 70
 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 75 80 85
 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Pro Asp Asn
 90 95 100 105
 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
 110 115 120
 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Val Ser Met
 125 130 135
 Val Phe

<210> 150
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 150
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 -20 -15 -10
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 -5 1 5
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 10 15 20 25
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 30 35 40

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 45 50 55
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 60 65 70
 Cys Ile Arg Ser Lys Asn Gly Pro Gly Thr Ala Val His Ala Tyr Asn
 75 80 85
 Pro Ser Thr Phe Arg Gly Gln Val
 90 95

<210> 151
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 151
 Met Val Glu Met Thr Gly Val
 1 5

<210> 152
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 152
 Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
 -40 -35 -30
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
 -25 -20 -15
 Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
 -10 -5 1 5
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
 10 15 20
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
 25 30 35
 Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
 40 45 50
 Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
 55 60 65 70
 Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
 75 80 85
 Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
 90 95 100
 Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
 105 110 115
 Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Val Leu Ala
 120 125 130
 Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 135 140 145 150
 Gly Leu Lys Arg Lys Ala Glu
 155

<210> 153

<211> 43
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Pro Phe Arg Met Ser Gly Tyr Ile Pro Phe Gly Thr Pro Ile Val
 1 5 10 15
 Ser Val Thr Phe Lys Gly Phe Pro Phe Leu Lys Asn Tyr Phe Lys Cys
 20 25 30
 Leu Thr Leu Cys Tyr Cys Ser Arg Val Phe Asp
 35 40

<210> 154
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 154
 Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
 -35 -30 -25
 Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
 -20 -15 -10
 Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5 1 5 10
 Gln Glu

<210> 155
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 155
 Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30
 Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
 35 40 45
 Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
 50 55 60
 Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
 65 70 75 80
 Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
 85 90 95
 Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
 100 105 110
 Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
 115 120 125
 Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
 130 135 140
 Gln Val Ser Gln Gln Glu Leu Lys
 145 150

<210> 156
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 156
 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Lys Leu Met Met
 1 5 10 15
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 20 25 30
 Gly Lys Asp Ile Asp Leu Asn Lys Val Arg Thr Lys Thr Ala Ala Lys
 35 40 45
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val
 50 55 60
 Pro Pro Glu
 65

<210> 157
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 157
 Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala Arg
 1 5 10 15
 Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val Phe
 20 25 30
 Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys Gly
 35 40 45
 Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln Ala
 50 55 60
 Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp Lys
 65 70 75 80
 Leu Ala Glu Glu His Ser Ser
 85

<210> 158
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -85...-1

<400> 158
 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
 -85 -80 -75 -70
 Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
 -65 -60 -55
 Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
 -50 -45 -40
 Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu Thr
 -35 -30 -25
 Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu Ala
 -20 -15 -10
 Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu Ala

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-5          1          5          10
Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val Tyr
      15          20          25
Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu Glu
      30          35          40
Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser Ala
      45          50          55
Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val Leu
60          65          70          75
Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu Gln
      80          85          90
Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu Lys
      95          100          105
Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Thr Ser Gln
      110          115          120
Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly Thr
      125          130          135
Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu Arg
140          145          150          155
Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn
      160          165

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<210> 159
 <211> 24
 <212> PRT
 <213> Homo sapiens

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<400> 159
Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
1          5          10          15
His Ile Asn Ile Ser Phe His Arg
      20

```

<210> 160
 <211> 228
 <212> PRT
 <213> Homo sapiens

```

<400> 160
Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
1          5          10          15
His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp Pro Lys Arg Arg
      20          25          30
Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe Val Pro Gly Lys
      35          40          45
His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser Cys Phe Asp Leu
50          55          60
Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val Pro Thr Ile Phe
65          70          75          80
Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys Ser Arg Asn Leu
      85          90          95
Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro Ser Ser Leu Lys
      100          105          110
Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His Ser Tyr Ala Phe
      115          120          125
Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys Leu Glu Lys Glu
      130          135          140
Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu Gln Lys Glu Arg

```

```

145          150          155          160
Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu Val Lys Asn Leu
          165          170          175
Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro
          180          185          190
Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln
          195          200          205
Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys
          210          215          220
Ser Thr Phe Ile
225

```

```

<210> 161
<211> 86
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -20...-1

```

```

<400> 161
Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
-20          -15          -10          -5
Leu Val Leu Ala Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
          1          5          10
Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
          15          20          25
Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
          30          35          40
Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
          45          50          55          60
Pro Ala Lys Leu Arg Gln
          65

```

```

<210> 162
<211> 44
<212> PRT
<213> Homo sapiens

```

```

<400> 162
Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn
1          5          10          15
Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp Val
          20          25          30
Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
          35          40

```

```

<210> 163
<211> 314
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -58...-1

```

<400> 163

```

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
      -55      -50      -45
Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly
      -40      -35      -30
Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
      -25      -20      -15
His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
      -10      -5      1      5
Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro
      10      15      20
Cys Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala
      25      30      35
Ile Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His
      40      45      50
Asn Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu
      55      60      65      70
Glu Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu
      75      80      85
Glu Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr
      90      95      100
Glu Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg
      105      110      115
Lys Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp
      120      125      130
Ala Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys
      135      140      145      150
Tyr Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg
      155      160      165
Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His
      170      175      180
Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro
      185      190      195
Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys
      200      205      210
Ile Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met
      215      220      225      230
Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile
      235      240      245
Glu Tyr Asp Tyr Thr Arg His Phe Thr Met
      250      255

```

<210> 164

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -80...-1

<400> 164

```

Met Arg Thr Arg Thr Thr Gly Asn Pro Arg Gly Leu His Asp Thr Phe
      -80      -75      -70      -65
Pro Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg
      -60      -55      -50
Thr Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala
      -45      -40      -35
Leu Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr

```

-30 -25 -20
 Gln Leu Gly Arg Gly Leu Leu Ser Ala Cys Ala Pro Trp Gly Asp Gly
 -15 -10 -5
 Ser Thr Gln Pro Val Pro Leu Cys Ser
 1 5

<210> 165
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 165
 Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
 -15 -10 -5 1
 Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
 5 10 15
 Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
 20 25 30
 His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
 35 40 45
 Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
 50 55 60 65
 Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu Thr Ser Glu Pro Leu
 70 75 80
 Thr Ala

<210> 166
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 166
 Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn
 -35 -30 -25
 Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly
 -20 -15 -10 -5
 Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe
 1 5 10
 His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His
 15 20 25
 Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly
 30 35 40
 Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 45 50 55

<210> 167
 <211> 351
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 167

```

Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
  -15                      -10                      -5
Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
  1                      5                      10                      15
Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
  20                      25                      30
Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
  35                      40                      45
Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
  50                      55                      60
Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Ser Pro Glu Pro
  65                      70                      75                      80
Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
  85                      90                      95
Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
  100                      105                      110
Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
  115                      120                      125
Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
  130                      135                      140
Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
  145                      150                      155                      160
Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
  165                      170                      175
Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
  180                      185                      190
Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
  195                      200                      205
Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
  210                      215                      220
Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
  225                      230                      235                      240
Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
  245                      250                      255
Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
  260                      265                      270
Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
  275                      280                      285
Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
  290                      295                      300
His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Cys
  305                      310                      315                      320
His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp Arg
  325                      330                      335

```

<210> 168

<211> 138

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 168

```

Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu
  -45                      -40                      -35
Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser
  -30                      -25                      -20
Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile
  -15                      -10                      -5                      1
Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu
      5                      10                      15
Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly Ile
      20                      25                      30
Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val Ser Gly Glu
      35                      40                      45
Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro Leu Gln Phe
50                      55                      60                      65
Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His Thr Asn Arg Arg Glu
      70                      75                      80
Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala
      85                      90

```

<210> 169

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -73...-1

<400> 169

```

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
      -70                      -65                      -60
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
      -55                      -50                      -45
Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
      -40                      -35                      -30
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
      -25                      -20                      -15                      -10
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
      -5                      1                      5
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
      10                      15                      20
Pro Leu Gly Thr Pro
      25

```

<210> 170

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68...-1

<400> 170

```

Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65                      -60                      -55

```

Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
 80 85 90
 Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
 95 100 105
 Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
 110 115 120
 Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
 145 150 155
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
 175 180

<210> 171
 <211> 350
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68...-1

<400> 171
 Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
 -65 -60 -55
 Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala

<400> 172															
Met	Pro	Glu	Gly	Pro	Glu	Leu	His	Leu	Ala	Ser	Gln	Phe	Val	Asn	Glu
			-65					-60					-55		
Ala	Cys	Arg	Ala	Leu	Val	Phe	Gly	Gly	Cys	Val	Glu	Lys	Ser	Ser	Val
		-50					-45					-40			
Ser	Arg	Asn	Pro	Glu	Val	Pro	Phe	Glu	Ser	Ser	Ala	Tyr	Arg	Ile	Ser
	-35					-30					-25				
Ala	Ser	Ala	Arg	Gly	Lys	Glu	Leu	Arg	Leu	Ile	Leu	Ser	Pro	Leu	Pro
-20					-15					-10					-5
Gly	Ala	Gln	Pro	Gln	Gln	Glu	Pro	Leu	Ala	Leu	Val	Phe	Arg	Phe	Gly
			1					5					10		
Met	Ser	Gly	Ser	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His
	15						20					25			
Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu
	30					35					40				
Cys	Phe	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys
45					50					55					60
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe
			65						70					75	
Arg	Glu	Asn	Val	Leu	Arg	Asn	Leu	Ala	Asp	Lys	Ala	Phe	Asp	Arg	Pro
		80						85					90		
Ile	Cys	Glu	Ala	Leu	Leu	Asp	Gln	Arg	Phe	Phe	Asn	Gly	Ile	Gly	Asn
	95						100					105			
Tyr	Leu	Arg	Ala	Glu	Ile	Leu	Tyr	Arg	Leu	Lys	Ile	Pro	Pro	Phe	Glu
	110					115					120				

Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp
 145 150 155
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe
 175 180 185
 Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
 190 195 200
 Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
 205 210 215 220
 Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
 225 230 235
 Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
 240 245 250
 Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
 255 260 265
 Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
 270 275 280
 Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
 285 290 295 300
 His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
 305 310 315
 Glu Gly Thr Ser Ala Ser
 320

<210> 173

<211> 190

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -82...-1

<400> 173

Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
 35 40 45
 Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
 65 70 75
 Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His
 80 85 90
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu

95

100

105

<210> 174
 <211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -232...-1

<400> 174
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
 -230 -225 -220
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 -215 -210 -205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 -200 -195 -190 -185
 Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
 -180 -175 -170
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 -165 -160 -155
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 -150 -145 -140
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 -135 -130 -125
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 -120 -115 -110 -105
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
 -100 -95 -90
 Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
 -85 -80 -75
 Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
 -70 -65 -60
 Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
 -55 -50 -45
 Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
 -40 -35 -30 -25
 Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
 -20 -15 -10
 Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
 -5 1 5
 Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
 10 15 20
 Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
 25 30 35 40
 Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys
 45 50

<210> 175
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 175
 Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu

```

      20      25      30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
      35      40      45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
      50      55      60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65      70      75      80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
      85      90      95
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
      100      105      110
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
      115      120      125
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
      130      135      140
His His Cys Val Arg Glu Gly Ser Gly
145      150

```

<210> 176
 <211> 49
 <212> PRT
 <213> Homo sapiens

```

<400> 176
Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
1      5      10      15
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
      20      25      30
Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe
      35      40      45
Cys

```

<210> 177
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

```

<400> 177
Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
      -20      -15      -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
      -5      1      5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
      10      15      20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25      30      35      40
Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn
      45      50      55
Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys
      60      65      70
Pro Pro Arg
      75

```

<210> 178
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 178
 Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro
 -35 -30 -25
 Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala Leu Leu
 -20 -15 -10
 Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys
 -5 1 5 10
 Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro
 15 20 25
 Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser
 30 35 40
 Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile
 45 50 55

<210> 179
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 179
 Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
 -20 -15 -10
 Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
 -5 1 5
 Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
 10 15 20 25
 Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
 30 35 40
 Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
 45 50 55
 Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
 60 65 70
 Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
 75 80 85
 Gln Lys Leu Ala Lys Lys Met Phe Phe
 90 95

<210> 180
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg


```

1           5           10           15
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
           20           25           30
Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu
           35           40           45
Thr Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
           50           55

```

<210> 181
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

```

<400> 181
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
           -10           -5           1
Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala
           5           10           15
Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
           20           25           30
Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
           35           40           45           50
Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
           55           60           65
Tyr Arg Ile Cys Asp Leu
           70

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<210> 182
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

```

<400> 182
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
           -55           -50           -45
Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
           -40           -35           -30
Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
           -25           -20           -15
Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
           -10           -5           1           5
Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
           10           15           20
Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
           25           30           35
Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
           40           45           50
Gln Gln Glu Ala Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
           55           60           65           70
Ser Leu Gln Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu

```

75 80 85
 Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys
 90 95 100
 Leu His Pro Trp Ala
 105

<210> 183
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 183
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 184
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 184
 Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu
 -20 -15 -10
 Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile
 -5 1 5 10
 Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Cys
 15 20 25
 Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys Ile Cys Cys Ser Ala Phe
 30 35 40
 Cys Gly Asn Ile Cys Met Ser Ile Leu
 45 50

<210> 185
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 185
 Met Leu Gly Ala Glu Thr Glu Glu Lys Leu Phe Asp Ala Pro Leu Ser
 1 5 10 15

```

Ile Ser Lys Arg Glu Gln Leu Glu Gln Gln Val Pro Glu Asn Tyr Phe
      20      25      30
Tyr Val Pro Asp Leu Gly Gln Val Pro Glu Ile Asp Val Pro Ser Tyr
      35      40      45
Leu Pro Asp Leu Pro Gly Ile Ala Asn Asp Leu Met Tyr Ile Ala Asp
      50      55      60
Leu Gly Pro Gly Ile Ala Pro Ser Ala Pro Gly Thr Ile Pro Glu Leu
      65      70      75      80
Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met
      85      90      95
Gly Tyr

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<210> 186
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

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<400> 186
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu
      -20      -15      -10
Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
      -5      1      5      10
Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
      15      20      25
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro
      30      35      40
Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys
      45      50      55
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr
      60      65      70      75
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg
      80      85      90

```

<210> 187
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44...-1

```

<400> 187
Met Cys Cys Tyr Cys Arg Ile Phe Cys Leu Arg Cys Thr Tyr Phe Pro
      -40      -35      -30
Val His Cys Gly Met Cys Asn Leu Arg Tyr Phe Glu Phe Ser Thr Phe
      -25      -20      -15
Leu Leu Ser Leu Ser Leu Ile Thr Tyr Cys Phe Trp Asp Pro Pro His
      -10      -5      1
Arg Gly Ser His Ser Leu Ser Leu Glu His Thr Pro Leu Asp Phe Leu
      5      10      15      20
Glu Trp Gly Leu Leu Arg
      25

```

<210> 188
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 188
 Met Leu Phe Ser Leu Ser Leu Leu Ser Asn Leu Asn Gln Ile Gly Ser
 -10 -5 1
 Ser His Leu Asp Arg Pro His Ile Pro Gly Gln Ser Ala Gln Leu Phe
 5 10 15
 Ile Tyr Gln Met Ser Ser Gln Gln Leu Gln Gln Gln Pro Ser Ala Asn
 20 25 30 35
 Lys Lys Ala Gly Lys Ile His Asn Thr Pro Phe Ala Asn Gln Leu Asn
 40 45 50
 Pro Thr Gln His Leu Ala Lys Pro Phe Gln Gln Ile Leu Pro Gly Arg
 55 60 65
 Gln Ser Gly Ser Leu Thr Ser Pro Phe Leu Ala Cys
 70 75

<210> 189
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 189
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
 -10 -5 1 5
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
 25 30 35
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
 40 45 50
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu
 55 60 65 70
 Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile
 75 80 85
 Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu
 90 95 100
 Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys
 105 110 115
 Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro
 120 125 130
 Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu
 135 140 145 150
 Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155

160

165

<210> 190
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala Leu Lys Glu Lys Phe
 1 5 10 15
 Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe Gln Glu Ile Pro Lys
 20 25 30
 Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln Leu Glu Lys Ile Glu
 35 40 45
 Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile Asn Ile Thr Glu Met
 50 55 60
 Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val Asn His Leu Lys Ala
 65 70 75 80
 Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu Pro Thr Thr Val Glu
 85 90 95
 Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn Thr Leu Asn Ser Val
 100 105 110
 His Leu Ala Val Glu Ala Leu Gln Lys Thr Val Asp Glu His Lys Lys
 115 120 125
 Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln His Phe Leu Lys Glu
 130 135 140
 Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro Ser Ala Thr Ser Glu
 145 150 155 160
 Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys Gln Met Gly Asp Arg
 165 170 175
 Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln Val Thr Asn Arg Thr
 180 185 190
 Asp Thr Val Lys Ile Gln Lys Lys Lys
 195 200

<210> 191
 <211> 379
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 191
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 -35 -30 -25
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 -20 -15 -10
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 -5 1 5 10
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 15 20 25
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 30 35 40
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 45 50 55
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

60				65				70				75			
Val	Gly	Pro	Pro	Phe	Thr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln
				80					85					90	
Ala	Leu	Asn	Ile	Leu	Leu	Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile
		95						100					105		
Ser	Ala	Val	Cys	Glu	Lys	Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala
		110						115					120		
Trp	Ser	Tyr	Tyr	Ile	Gly	Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln
		125						130					135		
Ala	Arg	Ile	Arg	Thr	Tyr	Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly
140						145				150					155
Ala	Val	Ser	Gln	Arg	Leu	Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val
				160						165					170
Pro	Asp	Asn	Leu	Ser	Met	Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys
				175					180					185	
Leu	Pro	Gln	Gln	Thr	Gly	Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr
		190						195					200		
Ser	Asn	Ser	Ile	Tyr	Glu	Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr
		205						210					215		
Cys	Val	Leu	Glu	Tyr	Ala	Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser
220						225					230				235
Gln	Tyr	Ser	Gln	Ala	Gly	Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala
				240						245					250
Lys	Leu	Phe	Cys	Arg	Thr	Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu
				255					260					265	
Ser	Gln	Asn	Asn	Cys	Arg	Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp
		270						275					280		
Ser	Ser	Phe	Ser	Leu	Ser	Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu
		285						290					295		
Glu	Lys	Glu	Glu	Val	Thr	Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro
300						305					310				315
Ser	Thr	Ser	Thr	Met	Ser	Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met
				320						325					330
Gly	Lys	Pro	Leu	Pro	Leu	Arg	Thr	Asp	Phe	Ser					
			335						340						

<210> 192

<211> 112

<212> PRT

<213> Homo sapiens

<400> 192

Met	Pro	Ser	Glu	Gly	Arg	Cys	Trp	Glu	Thr	Leu	Lys	Ala	Leu	Arg	Ser
1				5					10					15	
Ser	Asp	Lys	Gly	Arg	Leu	Cys	Tyr	Tyr	Arg	Asp	Trp	Leu	Leu	Arg	Arg
		20						25					30		
Glu	Asp	Val	Leu	Glu	Glu	Cys	Met	Ser	Leu	Pro	Lys	Leu	Ser	Ser	Tyr
		35					40					45			
Ser	Gly	Trp	Val	Val	Glu	His	Val	Leu	Pro	His	Met	Gln	Glu	Asn	Gln
		50				55					60				
Pro	Leu	Ser	Glu	Thr	Ser	Pro	Ser	Ser	Thr	Ser	Ala	Ser	Ala	Leu	Asp
65					70					75				80	
Gln	Pro	Ser	Phe	Val	Pro	Lys	Ser	Pro	Asp	Ala	Ser	Ser	Ala	Phe	Ser
			85						90					95	
Pro	Ala	Ser	Pro	Ala	Thr	Pro	Asn	Gly	Thr	Lys	Gly	Lys	Lys	Lys	Lys
			100					105						110	

<210> 193

<211> 43
 <212> PRT
 <213> Homo sapiens

<400> 193
 Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly Ser
 1 5 10 15
 Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg Asn
 20 25 30
 Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
 35 40

<210> 194
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 194
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 195
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 195
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
 -15 -10 -5
 Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
 1 5 10
 Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
 15 20 25 30
 Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
 35 40 45
 Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp
 50 55 60
 Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
 65 70 75
 Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
 80 85 90
 Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
 95 100 105 110
 Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr

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      115      120      125
Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro
      130      135      140
Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln
      145      150      155
Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp
      160      165      170
Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro
      175      180      185      190
His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu Val
      195      200      205
Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly
      210      215      220
Arg Thr Ala Trp
      225

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<210> 196
 <211> 353
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

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<400> 196
Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
      -30      -25      -20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
      -15      -10      -5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
      1      5      10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
      15      20      25      30
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
      35      40      45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
      50      55      60
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr
      65      70      75
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr
      80      85      90
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly
      95      100      105      110
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met
      115      120      125
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
      130      135      140
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
      145      150      155
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
      160      165      170
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
      175      180      185      190
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
      195      200      205
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
      210      215      220
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
      225      230      235

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Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
 240 245 250
 Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
 255 260 265 270
 Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
 275 280 285
 Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
 290 295 300
 Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
 305 310 315
 Leu

<210> 197
 <211> 30
 <212> PRT
 <213> Homo sapiens

<400> 197
 Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His
 1 5 10 15
 Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys
 20 25 30

<210> 198
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 198
 Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
 -45 -40 -35
 Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
 -30 -25 -20
 Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
 -15 -10 -5
 Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
 1 5 10 15
 Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
 20 25 30
 Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser
 35 40 45
 Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
 50 55 60

<210> 199
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 199
 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15

Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 Ser Ser Gly His Leu Pro
 50

<210> 200
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 200
 Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr Ala Ala Val
 -20 -15 -10
 Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
 -5 1 5 10
 Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
 15 20 25
 Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
 30 35 40
 Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Ile Thr Glu Glu Asp
 45 50 55
 Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
 60 65 70 75
 Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ser Lys
 80 85 90
 Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 201
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 201
 Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
 -25 -20 -15 -10
 Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
 -5 1 5
 Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu
 10 15 20
 Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu
 25 30 35
 Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala
 40 45 50 55

Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Leu Gly
 60 65 70
 Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg
 75 80 85
 Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro His Ile Leu Ala Gly
 90 95 100
 Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg
 105 110 115
 Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro
 120 125 130 135
 Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly
 140 145 150
 Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Pro Ala
 155 160 165
 Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val
 170 175 180
 Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
 185 190 195
 Asn Ala Tyr Val
 200

<210> 202

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 202

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
 -45 -40 -35
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
 -30 -25 -20
 Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
 -15 -10 -5 1
 Pro Asp Leu Pro Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
 5 10 15

<210> 203

<211> 146

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31...-1

<400> 203

Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly
 -30 -25 -20
 Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile
 -15 -10 -5 1
 Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys
 5 10 15
 Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu
 20 25 30

Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn
 35 40 45
 Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile Pro Val Ser Gly Ser
 50 55 60 65
 Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg Gly Gly Pro Phe
 70 75 80
 Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu Lys Asp Gly Gln
 85 90 95
 Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly Asp Glu Val Lys
 100 105 110
 Lys Glu
 115

<210> 204
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser Leu
 1 5 10 15
 Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His Leu
 20 25 30
 Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro Glu
 35 40 45
 Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln Ser
 50 55 60
 Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu Leu
 65 70 75 80
 Glu Val Asp Asp Trp Glu Phe
 85

<210> 205
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 205
 Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 Leu Ser Leu Arg Ser Ala Met Ser
 10

<210> 206
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg

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1           5           10           15
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
      20           25           30
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
      35           40           45
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
      50           55           60
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
      65           70           75           80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
      85           90           95
Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
      100           105           110
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
      115           120           125
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
      130           135           140
Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
      145           150

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<210> 207
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 207
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
1           5           10           15
Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
      20           25           30
Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
      35           40           45
Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
      50           55           60
Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
      65           70           75           80
Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
      85           90           95
Lys Gln Thr Ser Val
      100

```

<210> 208
 <211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

```

<400> 208
Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly
      -20           -15           -10
Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn
      -5           1           5           10
Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu
      15           20           25
Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser

```


<400> 209

```

Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp
      -15                      -10                      -5
Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp
  1          5          10          15
Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser
      20          25          30
Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile
      35          40          45
Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe
  50          55          60
Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln
  65          70          75
Val Glu
80

```

<210> 210

<211> 83

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29...-1

<400> 210

```

Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
      -25                      -20                      -15
Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
      -10                      -5                      1
Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
  5          10          15
Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
  20          25          30          35
Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
      40          45          50
Asn Ala Ser

```

<210> 211

<211> 229

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 211

```

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Ala Ala
      -20          -15          -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
      -5          1          5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
  10          15          20          25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
      30          35          40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

```

```

      45      50      55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
      60      65      70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
      75      80      85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
90      95      100      105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
      110      115      120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
      125      130      135
Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
      140      145      150
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
      155      160      165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
170      175      180      185
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
      190      195      200
Arg Lys Ser Arg Thr
      205

```

<210> 212
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

```

<400> 212
Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
      -20      -15      -10
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
-5      1      5      10
Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly
      15      20      25
Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr
      30      35      40
Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly
      45      50      55
Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val
60      65      70      75
Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
      80      85      90
Lys Ala Leu Ile Phe Asn Lys Ile His Glu Leu Asn Gln Phe Cys
      95      100      105
Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu
      110      115      120
Asn Asp Phe Ser Gln Glu Ser Ser
      125      130

```

<210> 213
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -54...-1

<400> 213

```

Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
      -50                      -45                      -40
Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
      -35                      -30                      -25
Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala
      -20                      -15                      -10
Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
      -5                      1                      5                      10
Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
      15                      20                      25
Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu
      30                      35                      40
Ala Gly Met Pro Ser Pro Glu Trp Thr Lys Arg Lys Lys Gln Thr Leu
      45                      50                      55
Lys Ile Gly His Gly Gly Thr Leu Asp Ser Ala Ala Arg Gly Val Leu
      60                      65                      70
Val Val Gly Ile Gly Ser Gly Thr Lys Met Leu Thr Ser Met Leu Ser
      75                      80                      85                      90
Gly Ser Lys Arg Tyr Thr Ala Ile Gly Glu Leu Gly Lys Ala Thr Asp
      95                      100                      105
Thr Leu Asp Ser Thr Gly Lys Val Thr Glu Glu Lys Pro Tyr Gly Met
      110                      115                      120
Asn Leu Ile
      125

```

<210> 214

<211> 269

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -92...-1

<400> 214

```

Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu
      -90                      -85                      -80
Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro
      -75                      -70                      -65
Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp
      -60                      -55                      -50                      -45
Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr
      -40                      -35                      -30
Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala
      -25                      -20                      -15
Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val
      -10                      -5                      1
Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val
      5                      10                      15                      20
Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr Phe
      25                      30                      35
Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu Cys
      40                      45                      50
His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu Thr
      55                      60                      65

```

```

Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn
 70                      75                      80
Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala
85                      90                      95                      100
Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln
                      105                      110                      115
Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys Leu
                      120                      125                      130
His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala Asp
                      135                      140                      145
Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu Thr
                      150                      155                      160
Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
165                      170                      175

```

<210> 215
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

```

<400> 215
Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val
      -20                      -15                      -10
Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala
      -5                      1                      5                      10
Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser
                      15                      20                      25
Phe Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile
                      30                      35                      40
Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe
                      45                      50                      55
His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu
                      60                      65                      70
Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile
75                      80                      85                      90
Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn
                      95                      100                      105
Ser Ala Pro Lys Ser Asn Val
                      110

```

<210> 216
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

```

<400> 216
Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
      -35                      -30                      -25
Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr
      -20                      -15                      -10

```

Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 -5 1 5 10
 Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 15 20 25
 Glu Val Leu

<210> 217
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 217
 Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 -50 -45 -40
 Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
 -35 -30 -25
 Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
 -20 -15 -10
 Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
 -5 1 5 10
 Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
 15 20 25
 Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
 30 35 40
 Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
 45 50 55
 Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
 60 65 70

<210> 218
 <211> 376
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 218
 Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Pro Pro
 -20 -15 -10
 Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
 -5 1 5 10
 Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly
 15 20 25
 Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu
 30 35 40
 Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg
 45 50 55
 Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly
 60 65 70 75
 Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe
 80 85 90
 Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln Thr Lys

```

          95              100              105
Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys Leu Leu
      110              115              120
Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly Thr Leu
      125              130              135
Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala Val Asp
140              145              150              155
Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala Leu Thr
      160              165              170
Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp Asn His
      175              180              185
Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp Leu Val
      190              195              200
Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser Trp Leu
      205              210              215
Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe Gln Val
220              225              230              235
Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys Pro Trp
      240              245              250
Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro Val Ala
      255              260              265
Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg Ile Gln
      270              275              280
Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro Leu Pro
      285              290              295
Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val Ser Gly
300              305              310              315
Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly Gly His
      320              325              330
Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu Ala Gln
      335              340              345
Arg Ser Tyr Leu Pro Gln Ile Ser
      350              355

```

<210> 219

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30...-1

<400> 219

```

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
-30              -25              -20              -15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
      -10              -5              1
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
      5              10              15
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
      20              25              30
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
35              40              45              50
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
      55              60              65
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val Pro Arg Met
      70              75              80
Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe
      85              90              95

```

His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
 100 105 110
 Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
 115 120 125 130
 Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
 135 140 145
 Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser
 150 155 160
 Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
 165 170 175
 Arg Gln Leu
 180

<210> 220
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 220
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu
 25 30 35
 Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
 40 45 50
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe
 55 60 65
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
 70 75 80
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile
 85 90

<210> 221
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 221
 Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
 -40 -35 -30
 Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
 -25 -20 -15

```

Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met
-10          -5          1          5
Lys Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser
      10          15          20
Asp Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser
      25          30          35
Pro Arg Ile Ser Cys His Gly Ala Ala Ile Pro Thr Ala Arg Ala Leu
      40          45          50
Cys Leu Gly Cys Ser Cys Cys Thr Glu Arg Leu Leu Pro Pro Pro
55          60          65          70
Ser Leu Leu Ser Leu Glu Ala Pro Ala Ser Thr
      75          80

```

<210> 222

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 222

```

Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln
      -15          -10          -5
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
      1          5          10
Val Asp Arg Ala Glu Val Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
      15          20          25
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
30          35          40          45
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
      50          55          60
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
      65          70          75
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
      80          85          90
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln
      95          100          105
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Leu Asp Tyr Val
110          115          120          125
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
      130          135          140
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
      145          150          155
Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
      160          165          170
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
      175          180          185
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
190          195          200          205
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
      210          215          220
His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
      225          230          235
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
      240          245          250
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
      255          260          265
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr

```

270 275 280 285
 Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
 290 295 300
 Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
 305 310 315
 Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
 320 325

<210> 223
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 223
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
 -20 -15 -10 -5
 Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
 Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
 Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
 30 35 40
 Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
 45 50 55 60
 Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
 65 70 75
 Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
 80 85 90
 Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
 95 100 105
 Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
 110 115 120
 Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
 125 130 135 140
 Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
 145 150 155
 His Leu Leu Ala Val Thr Lys Glu Ser Met Leu Pro Ala Gly Ala Glu
 160 165 170
 Ser Lys His Thr Ala Thr Pro Ala His Ala Cys Val Gln Thr Gly Lys
 175 180 185
 Pro Lys
 190

<210> 224
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 224
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser

```

-20          -15          -10          -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
      1          5          10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
      15          20          25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
      30          35          40
Asn Asp Ala Pro Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
45          50          55          60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
      65          70          75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
      80          85          90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
      95          100          105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
      110          115          120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
125          130          135          140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
      145          150          155
His Leu Leu Ala Asp Thr Met Leu
      160

```

<210> 225

<211> 227

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22...-1

<400> 225

```

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
      -20          -15          -10
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
      -5          1          5          10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
      15          20          25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
      30          35          40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
45          50          55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
60          65          70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
75          80          85          90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
      95          100          105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
      110          115          120
Ser Gly Phe His Arg Tyr Gln Phe Val Tyr Leu Gln Glu Gly Lys
125          130          135
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
140          145          150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
155          160          165          170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
      175          180          185

```


Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
 190 195 200
 Ala Ala Cys
 205

<210> 226
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 226
 Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
 -40 -35 -30
 Ala Arg Ser Leu Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
 -25 -20 -15 -10
 Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
 -5 1 5
 Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
 10 15 20
 Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
 25 30

<210> 227
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 227
 Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
 1 5 10 15
 Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
 20 25 30
 Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met Val Lys Lys Ile Ala
 35 40 45
 Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
 50 55 60
 Asn Leu Leu Glu Val Cys Lys Lys Lys
 65 70

<210> 228
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 228
 Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
 -15 -10 -5
 Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp

```

1           5           10           15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
           20           25           30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
           35           40           45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
           50           55           60
Lys Asn
65

```

<210> 229
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

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<400> 229
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
Ile Leu Ala Lys Lys Lys Lys
60

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<210> 230
 <211> 54
 <212> PRT
 <213> Homo sapiens

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<400> 230
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
Gly Arg Gly Arg Pro His
50

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<210> 231
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 231

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Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
      -10      -5      1
Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
      5      10      15
Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
      20      25      30
Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
      35      40      45      50
Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
      55      60      65
Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met
      70      75      80
Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu
      85      90      95
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly
      100      105      110
Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
      115      120      125      130
Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
      135      140      145
Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
      150      155      160
Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
      165      170      175
Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
      180      185      190
Gln Glu
195

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<210> 232

<211> 108

<212> PRT

<213> Homo sapiens

<400> 232

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Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1      5      10      15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
      20      25      30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
      35      40      45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
      50      55      60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
      65      70      75      80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
      85      90      95
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
      100      105

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<210> 233

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 233

Met	Ser	Ser	Gly	Arg	Leu	Arg	Trp	Leu	Met	Pro	Val	Ile	Pro	Ala	Leu
			-15				-10					-5			
Trp	Gly	Ala	Glu	Lys	Gly	Glu	Ser	Pro	Glu	Val	Ser	Ser	Phe	Glu	Thr
1					5						10				
Arg	Leu	Ala	Asn	Met	Ala	Lys	Pro	Cys	Leu	Tyr					
15					20					25					

<210> 234

<211> 36

<212> PRT

<213> Homo sapiens

<400> 234

Met	Ser	Ala	Arg	Ile	Pro	Phe	Tyr	Lys	Asp	Thr	Ser	Gln	Ile	Arg	Leu
1				5				10					15		
Gly	Ser	Thr	Ile	Ile	Pro	His	Phe	Asn	Leu	Ile	Thr	Phe	Val	Lys	Thr
			20					25					30		
Phe	Phe	Gln	Ile												
			35												

<210> 235

<211> 307

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 235

Met	Leu	Ala	Val	Ser	Leu	Thr	Val	Pro	Leu	Leu	Gly	Ala	Met	Met	Leu
			-10					-5					1		
Leu	Glu	Ser	Pro	Ile	Asp	Pro	Gln	Pro	Leu	Ser	Phe	Lys	Glu	Pro	Pro
5					10						15				
Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	Gln	Ala	Glu
20					25					30				35	
Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	Ala	His	Ile
				40				45						50	
Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	Val	Lys	Leu
			55					60					65		
Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	Gly	Pro	Cys
		70				75					80				
Lys	Thr	Arg	Asp	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile	Arg
		85			90						95				
Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Cys	Lys	Gly	Leu
100					105					110				115	
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
			120					125						130	
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
			135					140						145	

Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
 150 155 160
 Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp
 165 170 175
 Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
 180 185 190 195
 Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
 200 205 210
 Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
 215 220 225
 Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
 230 235 240
 Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
 245 250 255
 Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
 260 265 270 275
 Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala
 280 285 290
 Lys Lys Lys

<210> 236
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 236
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 237
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 237
 Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5
 Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro

1 5 10
Gln Leu Ser Asp Lys Val His Asn Asp Ile
15 20

<210> 238
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 238
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
30 35 40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg
45 50 55 60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
65 70 75
Thr Gly Ile Ser Leu Ile Leu Thr Ser Val Phe Phe Thr Trp Leu Ile
80 85 90
Ile Asp Lys Thr Thr
95

<210> 239
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37...-1

<400> 239
Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
-35 -30 -25
Gln His Xaa Xaa Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile
-20 -15 -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
-5 1 5 10
Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu
15 20 25
Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val
30 35 40
Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn
45 50 55
Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
60 65 70 75
His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr
80 85 90
Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe

	95		100		105										
His	Ala	Gly	Tyr	Ser	Leu	Lys	Lys	Arg	His	Phe	Phe	Gln	Asn	Leu	Gly
	110					115						120			
Ser	Ile	Leu	Thr	Tyr	Ala	Phe	Leu	Gly	Thr	Ala	Ile	Ser	Cys	Ile	Val
	125					130					135				
Ile	Gly														
140															

<210> 240
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 240																
Met	Gln	Phe	Val	Asn	Val	Gly	Tyr	Phe	Leu	Ile	Ala	Ala	Gly	Val	Val	
	-25					-20					-15					
Val	Leu	Ala	Leu	Gly	Phe	Leu	Gly	Cys	Tyr	Gly	Ala	Lys	Thr	Glu	Ser	
	-10					-5				1				5		
Met	Cys	Ala	Leu	Val	Thr	Phe	Phe	Phe	Ile	Leu	Leu	Leu	Ile	Phe	Ile	
			10					15					20			
Ala	Glu	Val	Ala	Ala	Val	Val	Ala	Leu	Val	Tyr	Thr	Thr	Met	Ala		
		25					30					35				
Glu	His	Phe	Leu	Thr	Leu	Leu	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr		
	40					45					50					
Gly	Ser	Gln	Glu	Asp	Phe	Thr	Gln	Val	Trp	Asn	Thr	Thr	Met	Lys	Gly	
	55					60				65						
Leu	Lys	Cys	Arg	Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp	Ser	Pro	
70					75					80					85	
Tyr	Phe	Lys	Met	His	Lys	Pro	Val	Thr	Met	Lys	Lys	Lys	Lys			
				90					95							

<210> 241
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -115...-1

<400> 241																
Met	Arg	Trp	Ser	Cys	Glu	His	Leu	Val	Met	Val	Trp	Ile	Asn	Ala	Phe	
-115					-110				-105					-100		
Val	Met	Leu	Thr	Thr	Gln	Leu	Leu	Pro	Ser	Lys	Tyr	Cys	Asp	Leu	Leu	
			-95					-90					-85			
His	Lys	Ser	Ala	Ala	His	Leu	Gly	Lys	Trp	Gln	Lys	Leu	Glu	His	Gly	
	-80					-75						-70				
Ser	Tyr	Ser	Asn	Ala	Pro	Gln	His	Ile	Trp	Ser	Glu	Asn	Thr	Ile	Trp	
	-65				-60						-55					
Pro	Gln	Gly	Val	Leu	Val	Arg	His	Ser	Arg	Cys	Leu	Tyr	Arg	Ala	Met	
	-50				-45					-40						
Gly	Pro	Tyr	Asn	Val	Ala	Val	Pro	Ser	Asp	Val	Ser	His	Ala	Arg	Phe	
-35			-30						-25					-20		
Tyr	Phe	Leu	Phe	His	Arg	Pro	Leu	Arg	Leu	Leu	Asn	Leu	Leu	Ile	Leu	

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          -15          -10          -5
Ile Glu Gly Gly Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg Ser
      1          5          10
Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys Asn
      15          20          25
Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Ile Val Leu Gly Arg
      30          35          40          45
Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn
          50          55

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<210> 242
 <211> 896
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..173

<221> sig_peptide
 <222> 18..77
 <223> Von Heijne matrix
 score 6.5
 seq GLCVLQLTTAVTS/AF

<221> polyA_signal
 <222> 864..869

<221> polyA_site
 <222> 882..893

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<400> 242
aaccttcaca gtgtgag atg cct agt gtg aac agt gct gga tta tgt gtc      50
              Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
              -20          -15          -10
ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg      98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
              -5          1          5
aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc      146
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala
              10          15          20
cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcctgattca      193
His His Phe Ile His Pro Cys Leu Asp
              25          30
aagtgttacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgcttcag      253
agagggcagc acttatacct ggtggtcttt ctgatggtca gttttattcc cctcctgaat      313
ccgaagcagg atctgaagaa gctgaagaaa aacaggacag tgagaaacca cttttagaac      373
tatgagtact acttttgtaa aatgtgaaaa accctcacag aaagtcacg aggcacaaaag      433
aggcaggcag tggagtctcc ctgtcgacag taaagttgaa atggtgacgt cactgctgg      493
ctttattgaa cagctaataa agatttatatt attgtaatac ctcacagacg ttgtaccata      553
tccatgcaca tttagttgcc tgcctgtggc tggttaaggta atgtcatgat tcatcctctc      613
ttcagtgaga ctgagcctga tgtgttaaca aataggtgaa gaaagtcctg tgctgtattc      673
ctaatacaaaa gacttaatat attgaagtaa cactttttta gtaagcaaga taccttttta      733
tttcaattca cagaatggaa tttttttggt tcatgtctca gatttatttt gtatttcctt      793
tttaacactc tacatttccc ttgtttttta actcatgcac atgtgctctt tgtacagttt      853
taaaaagtgt aataaaatct gacatgtcaa aaaaaaaaaa mcg      896

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<210> 243

<211> 851
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..595

<221> sig_peptide
 <222> 17..85
 <223> Von Heijne matrix
 score 3.70000004768372
 seq FLPLXRAFAACRG/CQ

<221> polyA_signal
 <222> 820..825

<221> polyA_site
 <222> 840..851

<400> 243

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aagggggcgt ggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc      52
                Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
                        -20                                -15

ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg      100
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
-10                                -5                                1                                5
gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga      148
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
                10                                15                                20
ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat      196
Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
                25                                30                                35
aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa      244
Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
                40                                45                                50
tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa      292
Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
                55                                60                                65
tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa      340
Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
70                                75                                80                                85
aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg      388
Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu
                90                                95                                100
aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg      436
Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala
                105                                110                                115
gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat      484
Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr
                120                                125                                130
tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg      532
Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met
                135                                140                                145
gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa      580
Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln
150                                155                                160                                165
aag aag agg agc aac taggagtcca ctctgaccca gccagagtcc aggtttccac      635
Lys Lys Arg Ser Asn
                170
aggaagcara tggagctcct ttcacagggg ctctgagaaa aactggagct gatctcaaga      695
agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggtag gtcttggggc      755

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actgtggggc gcctgcctgc tgatgtgggc tctaggccag cttgttgtca cgtaegtggg 815
 gtgaaataaa gcccaagcac tgggaaaaaa aaaaaa 851

<210> 244
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..334

<221> sig_peptide
 <222> 89..130
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AFTLXSLQALL/CV

<221> polyA_signal
 <222> 462..467

<221> polyA_site
 <222> 484..495

<400> 244
 agtaggaasg cgccgscctg ggaggcgcca cgtcccttgc sgccggcgga gagamatcgc 60
 ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg 112
 Met Ala Phe Thr Leu Xaa Ser Leu
 -10
 ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag 160
 Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu
 -5 1 5 10
 gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt 208
 Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly
 15 20 25
 gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att 256
 Gly Phe Gly Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile
 30 35 40
 cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca 304
 Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser
 45 50 55
 att gca att gtg tta ctt tta tta ttt gga tgaatwtcat tggagaaaat 354
 Ile Ala Ile Val Leu Leu Leu Phe Gly
 60 65
 ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatattt 414
 atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaaat aaaaccaggg 474
 tttctattta aaaaaaaaaa a 495

<210> 245
 <211> 884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..614

<221> sig_peptide

<222> 21..83

<223> Von Heijne matrix

score 10

seq LWALAMVTRPASA/AP

<221> polyA_signal

<222> 849..854

<221> polyA_site

<222> 873..884

<400> 245

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aataccttag accctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc      53
                Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
                -20                                -15
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca      101
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
-10                -5                                1                    5
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg      149
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu
                10                15                20
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga cgg      197
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg
                25                30                35
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa      245
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
                40                45                50
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt      293
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu
55                60                65                70
cgg gca agc ctg ttg gaa act car atg gag gag gat att ctg cas ctg      341
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu
                75                80                85
cag gca rag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca car      389
Gln Ala Xaa Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln
                90                95                100
aag gtg cta cgg gac agc gtg cag cgg cta daa ktc cag ctg arg asc      437
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa
                105                110                115
gcc tgg ctg ggc cct gcc tac cga aaa ttt gar gtc tta aag gcy ccc      485
Ala Trp Leu Gly Pro Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro
                120                125                130
cck gam aar car aac cac atc cta tgg gcc ctc aca ggc cac gtg cak      533
Pro Xaa Lys Gln Asn His Ile Leu Trp Ala Leu Thr Gly His Val Xaa
135                140                145                150
cgg car arg cgg gar atg gtg gca cag cag cwt ckg ctg cna car atc      581
Arg Gln Xaa Arg Glu Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile
                155                160                165
cag gar aaa ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac      634
Gln Glu Lys Leu His Thr Ala Ala Leu Pro Ala
                170                175
tgaggaccaa tcatgctgca aggaacactt ccacgccccg tgaggcccct gtgcagggag      694
gagctgacctg ttactggga tcagccaggg cgccgggccc cacttctgag cacagagcar      754
agacagacgc aggcggggac aaaggcagag gatgtagccc cattggggag ggggtggagga      814
aggacatgta ccctttcatr mctacacacc cctcattaaa gcavagtcgt ggcattctcaa      874
aaaaaaaaaa

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<210> 246

<211> 897

<212> DNA

aagggcggt	gcctagcacc	cggaagagcc	gtcaacttag	cgagcgcaac	aggctgccgc	60
tgaggagctg	gagctggttg	ggactgggcc	gca atg gac aag ctg aag aag gtg			114
			Met Asp Lys Leu Lys Lys Val			
			-55		-50	
ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt						162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val						
	-45		-40		-35	
gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg						210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala						
	-30		-25		-20	
tgt ttt gct ata gga att ctg tgc tca ctg ctg ggt act gtt ctg ctg						258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu						
	-15		-10		-5	
tgg gtg ccc agg aag gga cta cac ctg ttc gca gtg ttt tat acc ttt						306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe						
1	5		10		15	
ggt aat atc gca tca att ggg agt acc atc ttc ctg atg gga cca gtg						354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val						
	20		25		30	
aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc						402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile						
	35		40		45	
atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg						450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp						
	50		55		60	
cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca						498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala						
65	70		75		80	
ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg						546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val						
	85		90		95	
aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat						593
Lys Xaa Cys Phe Ala Val Cys Leu Ala						
	100		105			
gaagcttttg aaggcactat ggacagaagc tggtggacag ttttgtwact atcttcgaaa						653
cctctgtctt acagacatgt gcctttttatc ttgcagcaat gtgttgcttg tgattcgaac						713
atttgagggt tactttttgga agcaacaata cattctcgaa cctgaatgtc agtagcacag						773
gatgagaagt gggttctgta tcttgtggag tggaatcttc ctcatgtacc tgtttcctct						833
ctggatgttg tcccactgaa ttcccatgaa tacaaaccta ttcagcaaca gcaaaaaaaaa						893
aaaa						897

<210> 247
 <211> 518
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..397

<221> sig_peptide
 <222> 74..127
 <223> Von Heijne matrix
 score 7.69999980926514
 seq LLLLPVLGLLVSS/KT

<221> polyA_signal
 <222> 472..477

<221> polyA_site
 <222> 507..518

<400> 247
 aaagaaagag ctgcsgtgca ggaattcgtg tgccggattt ggtagctga gcccaccgag 60
 aggcgcctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg 109
 Met Lys Ala Leu Cys Leu Leu Leu Pro Val Leu
 -15 -10
 ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc 157
 Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
 -5 1 5 10
 aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata 205
 Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
 15 20 25
 agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg 253
 Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
 30 35 40
 gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc 301
 Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
 45 50 55
 gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag 349
 Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
 60 65 70
 tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc 397
 Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
 75 80 85 90
 tgaggtcgcg cgcagcgcgt gcacagcgcg ggcggaggcg gctccaggtc cggagggggtt 457
 gcggggggagc tggaaataaa cctggagatg atgatgatga tgatgatgga aaaaaaaaaa 517
 a 518

<210> 248
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 51..242

<221> sig_peptide
 <222> 51..116
 <223> Von Heijne matrix

score 6.5
seq SCLCPALFPGTSS/FI

<221> polyA_signal
<222> 319..324

<221> polyA_site
<222> 339..350

<400> 248
acgtcattcc aaaaccacac ccttgcaaag ctttgtactc cgcaccccag atg atc 56
Met Ile
tcc agg cag ctc aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc 104
Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro
-20 -15 -10 -5
ggg act tcc tcc ttt att gta gca ctc agc tcc cca gcc gat ctg tac 152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr
1 5 10
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa 200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys
15 20 25
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta 242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
30 35 40
tgattttgct gaatttttaa taaaatgaaa accataaatt acatratgct tttattgach 302
cttgacmact ggcctaaata aaaaractct gactcaaaa aaaaaaaaa 350

<210> 249
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..191

<221> sig_peptide
<222> 111..155
<223> Von Heijne matrix
score 5.80000019073486
seq FLXLMTLTTHVHS/SA

<221> polyA_signal
<222> 965..970

<221> polyA_site
<222> 986..996

<400> 249
atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggtga tttccgagct 60
cagcaatgct cagctcataa tgatgtcaag caccatggcc agttttatga atg ggy 116
Met Gly
-15
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag 164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys
-10 -5 1
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat 211
Pro Asn Glu Gln Pro Trp Leu Leu Asn
5 10
ggtagcggtt gctatacaga atctttggat atgtgcatca gtgggtttatg ccaaattggt 271

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ggctgcatc accagctggg aagcaccgtc aaggaarata actgtggggg ctgcaacrga 331
natgggtcca cctgccgggt ggtccgaggg cartataaat cccakctctc cgcaacccaaa 391
tcrgatgata ctgtgggtgc aattccctat ggaagtakac atattcgctt tgtcttaaaa 451
ggctcctgac acttatatct ggaarccawa accctccagg ggactaawgg tgaaaacagt 511
ctcasctcca caggaacttt ccttgtggac aattctagtg tggacttcca gaawtttcca 571
gacwdagaga tactgagaat ggctggacca ctcacagcag atttcattgt caawattcgt 631
aactcgggct ccgctgacag tacagtccag kkcattctct atcaacccat catccaccga 691
tggaggggara cggatttctt tccttgctca gcaacctgtg gaggagggtta tcagctgaca 751
tcggctgagt gctacgatct gaggagcaac cgtgtgggtg ctgaccaata ctgtcactat 811
taccagagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca 871
gccagggtcag tcaaatttgc tagttcattt gtcataaaca taactcaagt tccaaatagg 931
ttatttaaat taaaatgaaa cgttttaatt aaaaataaaa tgaaattaaa catcaaaaaa 991
aaaaa 996

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<210> 250

<211> 860

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 45..602

<221> sig_peptide

<222> 45..107

<223> Von Heijne matrix

score 8.5

seq LLTIVGLILPTRG/QT

<221> polyA_signal

<222> 828..833

<221> polyA_site

<222> 850..860

<400> 250

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acctctctcc acgaggctgc cggcttagga cccccagctc cgac atg tcg ccc tct 56
                                     Met Ser Pro Ser
                                     -20
ggt cgc ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga 104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
-15 -10 -5
gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act 152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ala Asp Ser Thr
1 5 10 15
atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca 200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
20 25 30
gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca 248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
35 40 45
cca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct 296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
50 55 60
cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc 344
Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro
65 70 75
act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac 392
Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa
80 85 90 95

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gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt ttc atg agg      440
Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg
      100                      105                      110
atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt      488
Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys
      115                      120                      125
tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg      536
Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Ser Pro Val
      130                      135                      140
gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag      584
Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu
      145                      150                      155
tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag      632
Ser Ile Arg Asn Arg Ser
      160                      165
ccccctgcc gctcaccgtg cccagcctcc tgcattcccct cgaagagcct ggccagagag      692
ggaagacaca gatgatgaag ctggagccag ggctgccggt ccgagtctcc tacctcccccc      752
aaccctgccc gccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc      812
tctgctaaga caaaaagtaa agcactgtgg tctttgcaaa aaaaaaaaaa      860

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<210> 251
 <211> 593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..560

<221> sig_peptide
 <222> 24..101
 <223> Von Heijne matrix
 score 10.3999996185303
 seq LLLLLCGPSQDQC/RP

<221> polyA_signal
 <222> 563..568

<221> polyA_site
 <222> 583..593

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<400> 251
aanccagctg csgccggcca gcc atg gag act gga gcg ctg cgg cgc ccg caa      53
      Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
      -25                      -20
ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc      101
Leu Leu Pro Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
      -15                      -10                      -5
cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc      149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
      1                      5                      10                      15
ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga      197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly
      20                      25                      30
cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag      245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu
      35                      40                      45
atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac      293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His
      50                      55                      60

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aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc      341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser
65              70              75              80
gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac      389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp
85              90              95
acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg      437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr
100            105            110
cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan      485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa
115            120            125
gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa      533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys
130            135            140
acc cac ttc tgc ctt tct att ana ctt taaataaact ctgaaracct      580
Thr His Phe Cys Leu Ser Ile Xaa Leu
145            150
gtaaaaaaaaaaa aaa      593

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<210> 252

<211> 1114

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 109..558

<221> sig_peptide

<222> 109..273

<223> Von Heijne matrix

score 3.70000004768372

seq VAFMLTLPILVCK/VQ

<221> polyA_site

<222> 1104..1114

<400> 252

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attagctstc caaggtctcc cccagcactg aggagctcgc ctgctgccct cttgcgcgcg      60
ggaagcagca ccaagttcac ggccaacgcc ttggcactag ggtccaga atg gct aca      117
                               Met Ala Thr
                               -55
aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga      165
Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg
-50              -45              -40
ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc      213
Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala
-35              -30              -25
aca gcc ggg gtt gtg acc tcg gtg gcc ttc atg ctg act ctc ccg atc      261
Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
-20              -15              -10              -5
ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act      309
Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr
1              5              10
cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc      357
Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe
15              20              25
gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc      405
Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe

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      30              35              40
ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat 453
Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His
45              50              55              60
gct gtc agt ctg acc aag ctc gtc cgg ggg agg aaa gcc cct ttc cct 501
Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro
      65              70              75
gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt 549
Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys
      80              85              90
tat cgc tat tgaatatatt gtccctgacca tgaataggac caacgtcaat 598
Tyr Arg Tyr
      95
gtcttttctg agctttccgc tctcgtcgc aatgaaaact ttgtcctcct gctcacctac 658
ktcctcttct tgatggcgct gaccttcctc wtgtcctcct tcaccttctg tggtkccttc 718
acgggctgga avagacatgg ggcccacatc tacctcasga tgctcskctc cattgccatc 778
tgggtggcct ggatcacctc gtcctgctt cctgactttg accgcraggg ggatgacacc 838
atcmtcarct ccgccttggs trcsaatggc tgggtgttcc tggtggctta tgtagtccc 898
gagttttggc tgctcacaaa gcaackaaac cccatggatt atcctgttga ggatgctttc 958
tgtaaaccctc aactcgtgaa gaagagctat ggtgtggrga acagagccta sktcaagag 1018
gaaatcactc aaggttttga agagacaggg gacacgctct atgcccccta ttccacacat 1078
tttcagctgc agaascagcc tccccaaaaa aaaaaa 1114

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<210> 253

<211> 1182

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..835

<221> sig_peptide

<222> 128..220

<223> Von Heijne matrix

score 4.69999980926514

seq LAVDSWWLDPGHA/AV

<221> polyA_signal

<222> 1145..1150

<221> polyA_site

<222> 1170..1181

<400> 253

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aagaactgcg tctcgcgacc caggcgcgagg ttcccggagg acagccaaca agcgatgctg 60
ccgccgccgt ttcctgattg gttgtgggtg gctacctctt cgttctgatt ggccgctagt 120
gagcaag atg ctg agc aag ggt ctg aag cgg aaa cgg gag gag gag gag 169
      Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
      -30              -25              -20
gag aag gaa cct ctg gca gtc gac tcc tgg tgg cta gat cct ggc cac 217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
      -15              -10              -5
gca gcg gtg gca cag gca ccc ccg gcc gtg gcc tct agc tcc ctc ttt 265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
      1              5              10              15
gac ctc tca gtg ctc aag ctc cac cac agc ctg cag vrr agt rag ccg 313
Asp Leu Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro
      20              25              30
gac ctg cgg cac ctg gtg ctg gtc atr aac act ctg cgg cgc atc cag 361

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Asp Leu Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln
      35              40              45
gcg tcc atg gca ccc gcg gct gcc ctg cca cct gtg cct acc cca cct      409
Ala Ser Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro
      50              55              60
gca gcc ccc ant gtg gct gac aac tta ctg gca agc tcg gac gct gcc      457
Ala Ala Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala
      65              70              75
ctt tca gcc tcc atg gcc arm ctc ctg gar gac ctc agc cac att gag      505
Leu Ser Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu
      80              85              90              95
ggc ctg agt cag gct ccc caa ccc ttg gca gac gag ggg cca cca ggc      553
Gly Leu Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly
      100              105              110
cgt agc atc ggg gga wca ccg ccc amc ctg ggt gcc ttg gac ctg ctg      601
Arg Ser Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu
      115              120              125
ggc cca gcc act ggc tgt cta ctg gac aat ggg ctt gag ggc ctg ttt      649
Gly Pro Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe
      130              135              140
gag_gat att gac acc tct atg tat gac aat gaa ctt tgg gca cca gcc      697
Glu Asp Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala
      145              150              155
tct gag ggc ctc aaa cca ggc cct gag gat ggg ccg ggc aag gag gaa      745
Ser Glu Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu
      160              165              170              175
gct ccg gag ctg gac gag gcc gaa ttg gac tac ctc atg gat gtg ctg      793
Ala Pro Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu
      180              185              190
gtg ggc aca cag gca ctg gag cga ccg ccg ggg cca ggg cgc      835
Val Gly Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
      195              200              205
tgagccctcg tgctggaatg gttgtctggt atctgaactg agcctgctgg ctggaccaac      895
tgtcctcgaa aagacacagc tggcttcctt agtacagaga acagggcttg ggccactttg      955
gagagacaga atctagtctt gggcaacttc acatccgtcc tctgtctca gggctggcag      1015
ggggagcctg gaattacccc ctagtgatgg aatgacaggg tctgggtgggg actgaattcc      1075
ctggccctgg ggtcatagct tgggctgttc cttctctgat acgggaagag acccaatcag      1135
atttttcaaa ttaaagccag tcctgggaaa tctcaaaaaa aaaaaaac      1182

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<210> 254

<211> 1073

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..505

<221> sig_peptide

<222> 59..358

<223> Von Heijne matrix

score 3.70000004768372

seq LASSFLFTMGGLG/FI

<221> polyA_signal

<222> 1042..1047

<221> polyA_site

<222> 1062..1073

<400> 254
actgttttngg ggagggcggt ggggcttgag gccgagaacg gcccttgctg ccaccaac 58
atg gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac 106
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100 -95 -90 -85
ctg aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act 154
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80 -75 -70
gtg tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata 202
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65 -60 -55
att tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat 250
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50 -45 -40
gaa cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat 298
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35 -30 -25
gga caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg 346
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20 -15 -10 -5
gga ggt tta ggt ttc ata atc ctg gac gga tcg aat gca cca aat atc 394
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
1 5 10
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc 442
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
15 20 25
cta twr agt ttt ttc ayg gct aga gta ttc atg aga atg aaa ctg ccg 490
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
30 35 40
ggc tat ctg atg ggt tagagtgcct ttgasaagaa atcagtggat actggatttg 545
Gly Tyr Leu Met Gly
45
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaatg tggaaaagaa 605
tgaagagcag cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga 665
ctagaatttc ttcttggtat taaagagaca agtttatcac agaatttttt ttcctgctgg 725
cctattgcta taccaatgat gttgagtggc attttctttt tagtttttca ttaaaatata 785
ttccatatct acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat 845
tttttgagaga tgacatttct gatttttcaga aattaacata aaatccagaa gcaagattcc 905
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag 965
agtgtgtgat ggtagattat ttcagatatg tatgtaaaac tgtttcctga acaataagat 1025
gtatgaacgg agcagaaata aatacttttt ctaattaaaa aaaaaaaaa 1073

<210> 255

<211> 818

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..207

<221> sig_peptide

<222> 1..147

<223> Von Heijne matrix
score 7.59999990463257
seq HLPFLLLLSCVGX/XP

<221> polyA_signal

<222> 784..789

<221> polyA_site

<222> 807..818

<400> 255

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atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat      48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
          -45                      -40                      -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg      96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
          -30                      -25                      -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg      144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
          -15                      -10                      -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat      192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
          1                      5                      10                      15
ttt ttt att cct gac tgagtcacca caccctctc ccctgatcaa agggaatatk      247
Phe Phe Ile Pro Asp
          20
artttttaat ttggatcgac tgaggtgccca ggagaaactg cagkcccagg tatccmvaca      307
gccaccagga tgggccctcg cccaccccc accgcctctk cccaccttt tocaacgtgt      367
tgcattgctgg gaactggggg gtgtggggga aggggctgcc ggcttctttc aggangctga      427
rgtttggar caaaatcaac ctgggaracc accccggccg cggcgctca gtggacaggt      487
gggargaaaa gaaaacttct taccttggar garggacatc cgccttcctt atccttagct      547
tttttggtgc tcctccccac tgcccccttt aatttatattg gttgtttgcg gaaggagggg      607
ggaagggggg aagctggggc gggaactgtc cgaggtgctg agctggggcg ggaccggaat      667
cctcccggtg gggtaccagg gactgagttg ggccctggggc cgtgtccaag gtgccaatga      727
tgccggccga cagarcgggc cgcactgtct gtctgtccgt ctgtcccga aagaactata      787
aagcgctgga agcgctgca aaaaaaaaaa a      818

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<210> 256

<211> 971

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..734

<221> sig_peptide

<222> 12..101

<223> Von Heijne matrix

score 4.80000019073486

seq ILFCVGAVGACTL/SV

<221> polyA_signal

<222> 914..919

<221> polyA_site

<222> 961..971

<400> 256

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aatacacaga a atg ggg act gcg agc aga agc aac atc gct cgc cat ctg      50
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu
          -30                      -25                      -20
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act      98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr
          -15                      -10                      -5
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag      146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu

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      1           5           10           15
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag      194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu
      20           25           30
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac      242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn
      35           40           45
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg      290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg
      50           55           60
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act      338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr
      65           70           75
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg      386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
      80           85           90           95
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta      434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Thr Thr Leu Val Val
      100           105           110
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct      482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala
      115           120           125
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc      530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe
      130           135           140
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata      578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile
      145           150           155
aaa gaa gac tca caa aag aag aag agt gct cgg cgt att ttt cag gaa      626
Lys Glu Asp Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu
      160           165           170           175
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa      674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln
      180           185           190
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac      722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn
      195           200           205
tat gaa agg cca tagaaacggt ttaattttca atgaagtcac tgaaaatcca      774
Tyr Glu Arg Pro
      210
actccaggag ctatggcagt gttaatgaac atatatcatc aggtcttaaa aaaaaataaa      834
ggtaaaactga aaagacaact ggctacaaag aaggatgcc a raatgtaagg aaactataac      894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa      954
tttgccaaaa aaaaaaw                                         971

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<210> 257

<211> 640

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 378..518

<221> sig_peptide

<222> 378..467

<223> Von Heijne matrix

score 5.5

seq SLMTCTTLINASA/IS

<221> polyA_signal
<222> 607..612

<221> polyA_site
<222> 628..640

<400> 257
 agcctgggta akgcccaaga tggctgtctt cgccttagta ctctgtgtgaa gttggcgggg 60
 acggttcctg tcatcttctt gggcttattt ggtgtgctgt tgaagggggg agactagaga 120
 aatggcaggg aacctcttat ccggggcagg taggcgcctg tgggactggg tgcctctggc 180
 gtgcagaagc ttctctcttg gtgtgcctag attgatcggg ataaggctca ctctcccgcc 240
 ccccaaagtg gttgatcgtt ggaacgagaa aagggccatg ttcggagtgt atgacaacat 300
 cgggatcctg ggaaactttg aaaagcaccc caaagaactg atcagggggc ccatatggct 360
 tcgaggttgg aaaggga atg aat tgc aac gtt gta tcc gaa aga gga aaa 410
 Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys
 -30 -25 -20
 tgg ttg gaa gta gaa tgt tgc ctg atg acc tgc aca acc tta ata aac 458
 Trp Leu Glu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn
 -15 -10 -5
 gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat 506
 Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp
 1 5 10
 aga aga gaa agc tgagaacttc ggaaaaggct catctgtcac cctggaraag 558
 Arg Arg Glu Ser
 15
 ggaaactgta cttttccctg tgaggaaacg gctttgtatt ttctctgtaa taaaatgggg 618
 cttcttttga aaaaaaaaaa aa 640

<210> 258
 <211> 745
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..304

<221> sig_peptide
 <222> 110..193
 <223> Von Heijne matrix
 score 4.59999990463257
 seq PLQWSLLVAVVAG/SV

<221> polyA_signal
 <222> 708..713

<221> polyA_site
 <222> 732..743

<400> 258
 acttccgcct ggcctgctc agcvcagctc cshgagccct gcccaaccatg gtgaacttgg 60
 gtctgtcccg ggtggacgac gccgtggctg ccaagcaccc ggcaccggc atg gcc ttt 118
 Met Ala Phe
 ggc ttg cag atg ttc att cag agg aag ttt cca tac cct ttg cag tgg 166
 Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp
 -25 -20 -15 -10
 agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg 214
 Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val
 -5 1 5
 acg aga gtg gag tgc gag aaa tgc aac aac ctc tgg ctc ttc ctg gag 262

```

Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu
  10                      15                      20
acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc      304
Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser
  25                      30                      35
taggagagct ccagcagggg cacagargat tgggggcagg argartcttg aacacakcct 364
tcattgcccc tgaccccagg cccaccctcc ccacacccta gggtagccca gtcgtatcct 424
ctgtccgcat gtgtggccag gcctgacaaa cmcctgcaga tggctgctgc cccaacctgg 484
gacctgcccc ggaggttga gcagaaaggg ctctccctgg ggtggtgttt ctctcttagg 544
gtattgggat gcatgttctg cactgccagc agagaggggtg tgtctggggg ccaccaccta 604
tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt cctttctagc ccctgcatct 664
ccaacaagtc caaggtgaca gctggtgcta ggggcgtggg gttaataaat ggcttatcct 724
tctctccaaa aaaaaaaaaam c                                     745

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<210> 259

<211> 637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 201..419

<221> sig_peptide

<222> 201..272

<223> Von Heijne matrix

score 6.40000009536743

seq LSYLPLWLGPWP/CS

<221> polyA_signal

<222> 601..606

<221> polyA_site

<222> 627..637

<400> 259

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acaaaatata attgcctcts ccctctccca ttttctctct tgggagcaat ggtcacagtc      60
cctggtacct gaaaaggtag ctaggtctag gcccttcttc cctttccctt cctctccctt      120
accccagaac tttggtccc tttcccttct ctctctggtg gctccaggag gcctgtgatc      180
cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc      233
                               Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe
                               -20                      -15
ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc      281
Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly
                               -10                      -5                      1
tct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg      329
Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg
                               5                      10                      15
ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar      377
Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa
                               20                      25                      30                      35
aac cak tat gav aak tgg ggg cag ggc aca cat tca tct ttg      419
Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu
                               40                      45
targaagggtc tggcctgggg tcrgggtgaag gagggcccag gtcagttctg ggggtccagt      479
gacctgcttt gccattctcc tgggtccgct gctgctccct gtttctggag ctggatgttc      539
cccacctggc agttgagctg cctgagccaa tgtgtctgtc tttggtaact gagtgaacca      599
taataaaggg gaacatttgg ccctgtgaaa aaaaaaaaaa                                     637

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<210> 260
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 123..302

<221> sig_peptide
 <222> 123..176
 <223> Von Heijne matrix
 score 4.30000019073486
 seq WTCLKSFPSPTSS/HA

<221> polyA_signal
 <222> 1279..1284

<221> polyA_site
 <222> 1301..1312

<400> 260
 aagagcatcc tgcgccccgg cgcgggggccc tgcggtagcc tcaggccccc cccctggacc 60
 cgccgcagag ccagtgcaga atacagaaac tgcagccatg accacgcacg tcaccctgga 120
 ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg 167
 Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
 -15 -10 -5
 acc agc agc cat gca tcg agc ctc cac ctt cct cca tca tgt acc agg 215
 Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
 1 5 10
 cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca 263
 Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
 15 20 25
 ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat 312
 Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
 30 35 40
 gctggaggaa ggacatgakt atgcggtcat gctgtacacc tggcgagct gttccccggc 372
 cattccccag gtgaaatgca acragcagcc caaccgakta raratctatg araaracagt 432
 araggtgctg gagccggagg tcaccaagct catgaagttc atgtattttc arcgcaaggc 492
 catcgagcgg ttctgcascg aggtgaagcg gctgtgccat gccgagcgca ggaaggactt 552
 tgtctctgag gcctacctcc tgacccttgg caagttcatc aacatgtttg ctgtcctgga 612
 tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc 672
 acagttcctg cggaagatgg cagatcccca gtctatccag gagtcgcaga acctttccat 732
 gttcctggcc aaccacaaca ggatcaccca gtgtctccac cagcaacttg aagtgatccc 792
 aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa 852
 gatgtacctg actcccagtg agaaacatat gctcctcaag gtaaaactcc cctgaggccg 912
 caccatgga gcctgggctt accctctcac cttcttctta ttaaaaatcc gttttaaaaa 972
 acaatgtttc ttttttctta aacattgata cagatcttac ggcacataat ggtttgtaac 1032
 ctgttccttt cctgtaatat aatataccgt agtcaccttt ccagatgtca ttaaggctat 1092
 ttctacaatg ttatgtgtaa tgactgcaa gtattctgtt gtattggaac attgtcatgt 1152
 aacatatccc ctgtggttgg atatttgcta aacttcattg aacacccttg tagcagtttt 1212
 tgtgcacatc tttttgtcaa ggcaaacttc ctagaagaga aattgctggc tcaaagggaa 1272
 aaacagaata aatcgttttt tttatttcaa aaaaaaaaaa ccc 1315

<210> 261
 <211> 1035
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 98..673

<221> sig_peptide

<222> 98..376

<223> Von Heijne matrix

score 5.59999990463257

seq VLLLRQLFAQAEK/WY

<221> polyA_site

<222> 1025..1035

<400> 261

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aattttcygt ggtccaacta ccctcggcga tcccaggctt ggcgggggcac cgcttggcct      60
ctcccgttcc tttaggctgc cgccgctgcc tgccgcc atg gca gag ttg ggc cta      115
                               Met Ala Glu Leu Gly Leu
                               -90

aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt      163
Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg
      -85                               -80                               -75

tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac      211
Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp
      -70                               -65                               -60

ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc      259
Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val
      -55                               -50                               -45                               -40

tct gaa gtc ctc aat gga tta caa gct gtg gtt cat agt gag gtg gaa      307
Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu
      -35                               -30                               -25

tct gag ctc atc aac act gcc tat acc aat gtg tta ctt ctg cga cag      355
Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Leu Arg Gln
      -20                               -15                               -10

ctg ttt gca caa gct gag aag tgg tat ctt aag cta cag aca gac atc      403
Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile
      -5                               1                               5

tct gaa ctt gaa aac cga gaa tta tta gaa caa ktt gca gaa ttt gaa      451
Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu Gln Xaa Ala Glu Phe Glu
      10                               15                               20                               25

aaa gca rav att aca tct tca aac aaa aag ccc atc tta dat gtc aca      499
Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys Pro Ile Leu Xaa Val Thr
      30                               35                               40

aas cca aaa ctt gct cca ctt aat gaa ggt gga aca gca aaa ctc cta      547
Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly Gly Thr Ala Lys Leu Leu
      45                               50                               55

aac aag gta ata tgt att att ttg aga aac gga aag tct ctc att ctg      595
Asn Lys Val Ile Cys Ile Ile Leu Arg Asn Gly Lys Ser Leu Ile Leu
      60                               65                               70

tcc tgt cat tgc cta ggg tgg aga aac aaa agt gga agg ttt gtt tca      643
Ser Cys His Cys Leu Gly Trp Arg Asn Lys Ser Gly Arg Phe Val Ser
      75                               80                               85

ggg cct ctg agg ata att agt cca ttg cag tagttttact tgatggtacc      693
Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
      90                               95

ccatggggcca gaagagggca tacttaacct tctagagagc ctgaagtagc tcctgatcac      753
accttttcaa ggtaaaagtga agagcatgaa attttggaca gcgtttattg atggacattt      813
aaagtttggt atctgcggta acaaggagaa gggtttttaa gtttataaaa attatttatc      873
aattagccgg gtgtggtggt acgtgcctat agtcagagct actcgggagg ctgaggcagg      933
agaattgctt gaacccggga ggtggagggt gcagtgaagc gagatcacgc cactgcactc      993
tagcctgggc gacagagcga gactccatct caaaaaaaaa aa      1035

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<210> 262
 <211> 696
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..463

<221> sig_peptide
 <222> 17..232
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LMGLALAVYKCQS/MG

<221> polyA_signal
 <222> 657..662

<221> polyA_site
 <222> 684..696

<400> 262
 actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act 52
 Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
 -70 -65
 atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc 100
 Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro
 -60 -55 -50 -45
 att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt 148
 Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
 -40 -35 -30
 tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg 196
 Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
 -25 -20 -15
 atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta 244
 Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
 -10 -5 1
 cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga 292
 Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
 5 10 15 20
 atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg 340
 Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
 25 30 35
 cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca 388
 Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
 40 45 50
 gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac 436
 Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
 55 60 65
 caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca 483
 Gln Lys Thr Leu Phe Ser Met Val Gly
 70 75
 atgtgcatat tacgacaaac acaaaaaaac tataccataa cccagggctg aaaataatgt 543
 aaaaaaacttt atttttgttt ccagtacaga gcaaaacaac aacaaaaaaa cataactatg 603
 taaacaaaaa aataactgct gctaaatcaa aaactgttgc agcatctcct ttcaataaat 663
 taaatggttg araacaatgc aaaaaaaaaa aaa 696

<210> 263
 <211> 868

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 263..481

<221> sig_peptide
<222> 263..322
<223> Von Heijne matrix
score 11.1999998092651
seq ILVVLMGLPLAQA/LD

<221> polyA_site
<222> 858..868

<400> 263
aagacacgcc tacgattaga ctcaggcagg cacctaccgg cgagcggccg crvgtgactc 60
ccaggcgcgg cggtagctca cggtagtgaa ggtcacaggg ttgcagcact ccagtagac 120
caggagctcc gggaggcagg gccggcccca cgctctctgc gcaccaccct gagttggatc 180
ctctgtgcgc caccctctgag ttggatccag ggctagctgc tgttgacctc ccactccca 240
cgctgccctc ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg 292
Met Thr Pro Leu Leu Thr Leu Ile Leu Val
-20 -15
gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt 340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10 -5 1 5
gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg 388
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met
10 15 20
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg 436
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met
25 30 35
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta 481
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val
40 45 50
tgatggctac tccaagcacg cgtccaccac ctctgtctgc cagtacgacc tctgcaacgg 541
caccggcctt gccaccccg caccctggc cctggccccc atcctcctgg ccaccctctg 601
gggtctcttc taaagccccc gaggcagacc cactcaagaa caaagctctc gagacacact 661
gctayaccct ckcaccckc tcaccctgcc tcaccctcca cactccctgc gacctcctca 721
gccatgcccc gggtcaggac tgtgggcaag aagacacccg acctccccca accaccacac 781
gacctcactt cgaggccttg acctttcgat gctgtgtggg atcccaaaaag tgtccggctt 841
tgatgggctg atcagcaaaa aaaaaaa 868

<210> 264
<211> 775
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..299

<221> sig_peptide
<222> 42..101
<223> Von Heijne matrix
score 5.40000009536743
seq WFFVHSSALGLVLA/PP

<221> polyA_site

<222> 762..775

<400> 264

aacgatacaaa atggtaggcc ttcatgtgag cagtdacta c atg aat ctt cat ttc	56
Met Asn Leu His Phe	
-20	
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca	104
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro	
-15 -10 -5 1	
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt	152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys	
5 10 15	
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc	200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr	
20 25 30	
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa	248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys	
35 40 45	
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg	296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg	
50 55 60 65	
cag tgaaactwkk ttcwcttcta aagcccttca tttccacaa ggттаagctc	349
Gln	
tcgaaacccc atttgatcct tggttcctat ttcgatcctc ctttggaatc tgaaaatcgg	409
tctccatgtt gtatgcaaat taaaakttgc cttgtttggt actcttccaa cacagggtat	469
cagggaraaa gaggccttat ctgttcctcc atccccctg ttttgacaga ctgctaagaa	529
ttcctcagga cttcctttgg ttggggattt tactttccca aaagtctgat ctgatttctt	589
tcaggggtag acaagcttgt cctagtgctc tgcttcaggt cttatcagaa gaaaccagg	649
aatagaaaag gtagatgcct tgacttttgt ccctgttggt gggactaaag tgttttttgc	709
cagaattgtc aaaagctccg gttcaaactc tgtagagttt catggaaaaa aaaaacaaa	769
aaaaaa	775

<210> 265

<211> 1075

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 198..431

<221> sig peptide

<222> 198..260

<223> Von Heijne matrix

score 6.90000009536743

seq LLACGSLLPGLWQ/HL

<221> polyA site

<222> 1064..1074

<400> 265

atatatttct	gaggcagtac	ccatctcact	tgtaaactta	aaagacaccg	cagagatttg	60
agggactcag	aagtcaaata	gagtaggtta	aaaacctctt	atttttcaaa	ttaattgttt	120
taagaaacaa	gcatacctgt	gtaagtgaag	tatcttaatt	tgtgttgaat	caagttagga	180
gacagagatt	ctcatga	atg tgt cct	gtg ttc tca	aag cag ctg	cta gcc	230
		Met Cys Pro Val	Phe Ser Lys	Gln Leu Leu	Ala	
		-20	-15			
tgt ggg tct	ctc cta cct	ggg tta tgg	cag cac ctc	aca gcc aat	cac	278
Cys Gly Ser	Leu Leu Pro	Gly Leu Trp	Gln His Leu	Thr Ala Asn	His	
-10	-5	1	5			

```

tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca      326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
      10                      15                      20
gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt      374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
      25                      30                      35
tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac      422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
      40                      45                      50
tct atc acc tagccattgt akccatacca agccgggctt cctacttccc      471
Ser Ile Thr
55
tctgctcccc ttggtttcct cctgtraart aaatctcaact gacccttgat gcasctccaa      531
gcatatataa tatatatata ataaaaccat abtctaaaaa attcaaacca ggawaaataa      591
asccaraaat ttgtatggga aaaatctgca caaatattatt tggccagcat ggttatcatg      651
gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca      711
actacttacc tctcaatacc aaaaargaag caggaggcaa aatctctcaw taatttcata      771
aaaacaattc ttakctgggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc      831
saggtgggag gatcatgagg tcgggagatc aamaccatcc tggctaacat ggtgaaaccc      891
catctctact aaaattacaa aaaatttrgt gggcgagggtg gcgggcacct gtggtcccag      951
ctactcgga ggctgaggca agagaatggt gtgaacccca gggggcggag cctgcagtga      1011
gctgagatcg caccactgca ctccagcctg ggcgacagtg agactccgtc tcaaaaaaaa      1071
aaah

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<210> 266

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 279..473

<221> sig_peptide

<222> 279..362

<223> Von Heijne matrix
 score 4.40000009536743
 seq SCFLVALIIWCYL/RE

<221> polyA_signal

<222> 944..949

<221> polyA_site

<222> 970..981

<400> 266

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agaatcgtgt cttgtgtgcc cggcgggcgg ggtgagctcc tcaaggtctc ggagggccga      60
gggcagacac cggcgggcgg gcggasgctt actgctctct ctcttccagg gccgtccggg      120
cgctgaggct cataggctgg gcttcccgaa gccttcatcc gttgcccggg tcccgggatc      180
gggcccaccc tgccgcccag gaagaggacg accctgaccg cccattgag ttttctcca      240
gcaaagccaa cctcaccgc tggtcggtgg gccatacc atg gga aag gga cat cag      296
                                Met Gly Lys Gly His Gln
                                -25

```

```

cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg      344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu
      -20                      -15                      -10

```

```

atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg      392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu
      -5                      1                      5                      10

```

```

aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag      440

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      85              90              95
gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg      434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu
      100              105              110
tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag      482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln
      115              120              125              130
tct att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctg ctt      530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu
      135              140              145
cac tgg caa ctg ctg gtc atg gtk atw ttt ggg ttt ttk gga aca att      578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile
      150              155              160
tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc gcc      626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly
      165              170              175
tct gac tac cga agt atc tgatctggtg tccgtgaggg gacacgtatg      674
Ser Asp Tyr Arg Ser Ile
      180
acctcagaaa cacagctgga cacagagctt ggtggaagaa gtcgcctttg atcttcacta      734
tatattgggt gatgttcagt atggaaaatc aagggattaa gactgttaaa tcagccagag      794
tkggtgttca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctgtt      854
ctgtcaactg taattgttca aagatgttgt ttttcatttc atctatctca attcttataa      914
tcatgttata gaatgtaaat gttttcttct ctctcctgct cttgttgga gacactgcct      974
tgatttagaa tactaggcca tatgtcatat aaatattttt tctggaaaaa aaaaaaa      1031

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<210> 268
 <211> 1283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..459

<221> sig_peptide
 <222> 91..330
 <223> Von Heijne matrix
 score 7.69999980926514
 seq LVLFLSLALLVTP/TS

<221> polyA_site
 <222> 1271..1281

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<400> 268
tattccttgg agttccacga ctgaattaag actggttggtg grdcataat tttcaaatac      60
ttgccctata ttcgtgttga gggttcacac atg agc aca tgg tat ttg gca ctt      114
                               Met Ser Thr Trp Tyr Leu Ala Leu
                               -80              -75
aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctg agc ttg      162
Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu
      -70              -65              -60
tgc aca gtg agc att aaa ttt aca tac ttt cat gat ata cag act aat      210
Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn
      -55              -50              -45
tgt ctt aca aca tgg aaa cat tcg aga tgc aga ttt tat tgg gca ttt      258
Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe
      -40              -35              -30              -25
ggg ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta      306
Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu

```



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                -20                -15                -10
agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata 354
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile
                -5                1                5
car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac 402
Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp
                10                15                20
agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt 450
Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu
                25                30                35                40
cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct 499
His Gln Leu
gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaaag 559
ctattaagtt attaagtgtc agccctggat cttggcttat tgtgaaatgt taattatattt 619
atcactcyat taagaagctg tgggctccat ctcagcattg aaaagggact aatttgctct 679
gtttttggaat tgaattagct ttcaggccas cagggcactg tttggtaaat tgctttttcc 739
agtactagca tgttttctcc ctccatagcc tctgttagct tctgagcttg taacctccag 799
ggaaavatga gaatattcac ctttttaata tgtgtagaga ccatgcaaga ccattgtctt 859
ctaataatta gaaatactta gccagattct ctatagtaaa cccggagatt gggagggtg 919
ctttctactt ggtgcaccc tctgcgcttc taatgatttt taaaaatctg ttaataattg 979
atgttttctg gctgggcaca gtggctcacg cctgtaatcc cagcactttg ggaggccaag 1039
gagggcagat catgagggtca ggagattgar accatcctgg ctaacacggt gaaaccccg 1099
ctctactaaa aatacaaaaar aattakccgg gcatggtagt gggcgctgt gtaccagct 1159
actggggagg ctgaggcarg araatcgctt gaacctggga ggcggagggtt gcastragct 1219
gagatggtgc caccgcactc tagcctgggt gacagagcga gacttcattt caaaaaaaaaa 1279
aamc 1283

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<210> 269

<211> 1777

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..327

<221> sig_peptide

<222> 70..147

<223> Von Heijne matrix

score 9.60000038146973

seq WLIALASWSWALC/RI

<221> polyA_signal

<222> 1741..1746

<221> polyA_site

<222> 1763..1774

<400> 269

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agccccggttt cgtgcccgcg gccgactgcg casctgtccg cgagtctgag atacttacag 60
agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg 111
Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp
                -25                -20                -15
cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt 159
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu
                -10                -5                1
tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt 207
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu
                5                10                15                20
ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat 255

```

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Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp
      25              30              35
gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat      303
Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp
      40              45              50
tcc cat gcc cac tgg cmt tcg rca taaaaaaatt ttcacacagaa ccaaagatgg      357
Ser His Ala His Trp Xaa Ser Xaa
      55              60
aatacgtctg aatcttattt tgatacgata cactggagac aattcacccct attccccaac      417
tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac      477
ttatgttggt taacctcaaa gttaaccttt tgctgggtga ttatcgagga tatggaaaaa      537
gtgaaggaga agcaagtga gaaggactct acttagattc tgaagctgtg ttagactacg      597
tgatgactag acctgacctt gataaaaacaa aaatttttct ttttggccgt tccttgggtg      657
garcagtggc tattcatttg gcttctgaaa attcacatag gatttcagcc attatgggtg      717
agaacacatt ttttaagcata ccacatatgg ccagcacttt attttcattc tttccgatgc      777
gttaccttcc tttatgggtg tacaaaaata aatttttgtc ctacagaaaa atctctcagt      837
gtagaatgcc ttcacttttc atctctggac tctcagatca attaatcca ccagtaatga      897
tgaaacaact ttatgaactc tccccatctc ggactaagan attagccatt tttccagatg      957
ggactcacia tgacacatgg cagtgccaaag gctattttcac tgcacttgaa cagttcatca      1017
aagaagtcgt aaagagccat tctcctgaag aaatggcaaa aacttcactc aatgtaacaa      1077
ttatataatg tttccctttt tgattattgc attgtatttt aatttgtgca gaatgataaa      1137
gaatgttctt tttagaagtg tgttatgtct gtacctgtct gaagagtgc attaaacttt      1197
gaaaggactt cactgtctct ttacgatatt ccaaatagtt ttttacattg gaaaaactaa      1257
ttcttgggat tctttcatac attttcatca aaactttcag tgtgattatg tattcatatc      1317
ttcagtttaa tatgtcagta taatagatat tgttcaaaag tttcttgttg ctaaagtggg      1377
gtaatctgtt acacagatga atagctagat gtggaaagag atatgtaaac aagaaacctt      1437
tggttattgt ttcttaagta aatattggga caatcatggg aagcaaactt agttctgtaa      1497
ctgcattttt caccttaaaa gttaaatgaa atgcatgatg gtattttatt ccttgaatta      1557
tgcaatgcaa cattttacat gttaaatgca ctggtcatat actgatgtat atgggttatct      1617
gggttatatc tatttttatg taaactctat ttttgtttt ggcaagaagt gaaattgaga      1677
cttatgtgca ggttgccatt gaattttgct ctggtgaatg ctgagatcca gctttttctt      1737
acaaataaat gggaccctgt tttccaaaaa aaaaaaamcm      1777

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<210> 270

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..497

<221> sig_peptide

<222> 12..104

<223> Von Heijne matrix

score 5.5

seq LVGVLWVSVTTG/PW

<221> polyA_signal

<222> 935..940

<221> polyA_site

<222> 955..967

<400> 270

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aggtctccaa g atg gcg gcc gcc tgg ccg tct ggt ccg kct gct ccg gag      50
      Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
      -30              -25              -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act      98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr

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      -15      -10      -5
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg      146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
      1      5      10
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
      15      20      25      30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
      35      40      45
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
      50      55      60
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
      65      70      75
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
      80      85      90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tcg att tta cct tgg      434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
      95      100      105      110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg      482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
      115      120      125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca      537
Asn Trp Glu Pro Asn
      130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact      597
aatgaaacat ttagaaaaac gcaattatat ccataaatat tttttaaaag aaacagattt      657
gagcctcctt gattttaata gagaacttct agtgtatgga tttaaagatt tctctttttc      717
attcatatac cattttatga gttctgtata attttttgtg gtttttgttt tggtgagtta      777
aagtatatta ttgtgagatt tatttaatag gacttccttt gaaagctgta taatagtgtt      837
tctcgggctt ctgtctctat gagagatagc ttattactct gatactcttt aatcttttac      897
aaaggcaagt tgccacttgt catttttggt tctgaaaaat aaaagtataa cttattcaca      957
aaaaaaaaaa mms      970

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<210> 271
 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..383

<221> sig_peptide
 <222> 90..200
 <223> Von Heijne matrix
 score 4.90000009536743
 seq MLIMLGIFNVHS/AV

<221> polyA_signal
 <222> 609..614

<221> polyA_site
 <222> 632..643

<400> 271
 atctctgccc ccctgcgagg gcatactggg ctttctccca ccgctttccg agcccgtttg 60

[illegible]

```

ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca      448
Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser
  10                      15                      20
ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac      496
Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr
  25                      30                      35                      40
ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act      541
Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr
      45                      50                      55
tgaaaagaaa gtgtttttatt ttcaaattctg gtccatatatt acatttctagt tcagagccaa      601
gccttaaaact gtacagaatt tccactgtaa ttaaaactat ttagtggttag ttataaatag      661
ccttcaaaaa gagagattct ccattacacg atcacctgca tcacagccca tggatgaatgt      721
atgtttctgc atagcgaaat aaaaatggca aatgcactga aaaaaaaaaa aa      773

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<210> 273

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 43..222

<221> sig_peptide

<222> 43..177

<223> Von Heijne matrix

score 4

seq ENFLSLLSKSCSA/DP

<221> polyA_signal

<222> 530..535

<221> polyA_site

<222> 555..566

<400> 273

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aacgagtgga ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt      54
                                     Met His Ser Leu
                                     -45
ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg      102
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg
  -40                      -35                      -30
ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt      150
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu
  -25                      -20                      -15                      -10
agc ctt ctc agc aaa agt tgt tct gcg gac ccg tct ggg tca act ttc      198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe
      -5                      1                      5
atg agg gac att gag aca aac aaa tgaaatatgg gttaaagtac tctgagcagc      252
Met Arg Asp Ile Glu Thr Asn Lys
  10                      15
tacaaaaaga araccagtct atcctgtctgg agacagtggc cacgtgaara aagagctctt      312
gcagtatgaa agaccacatg gaaagagagg ccacatggaa ccaacagtca gcatcttggt      372
ttcggacacg tgaaraaatt catctcarac tgtgtatcct aaatcaggca cttgtgtaat      432
ctaactacat gaggtagacc agttgacaac acatggagca racatgagct gttctcagtg      492
artcctacac aaattcctga ctcaaacac tgtgagcaat aaaatgggtg ttattttaag      552
ccaaaaaaaa aaaa      566

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<221> polyA_site
<222> 662..673
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<400> 275

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atttggttg cagactgcct tctatcccag aacagctgag aaatctatga agctgagatt 60
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agccttagtt tcccatggcc ctgaaacaca cacatttccc ccttcctttc ccagaagcca 180
ctggccccc atagcaccca gtgcctcctt tttacaagtg gaagaactag g atg gct 237
                                     Met Ala
ttc caa agt ctt cta gaa atg aag ttc ttt ctc tgt gca gct ttc ccc 285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
-20 -15 -10
ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca 333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
-5 1 5 10
ctt cyy cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg 381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
15 20 25
cct tagcttctgg gcctatcsgc tgccttcctt cttyttccta ccacctcttc 434
Pro
tgccttcctt trawctctgt tgggcttggt gatcttagtt ttcttttggt tatttcccat 494
ctcatttttt tcttctggtc agttttttta agggggggtg ttgtgggttt ttgtttttgt 554
tttgcttctg aaaaarcatt tgcctttcct cctctcccaa cataacaatc gtggtaacag 614
aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa 673

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<210> 276

<211> 639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 143..427

<221> sig_peptide

<222> 143..286

<223> Von Heijne matrix

score 7.5

seq FVILLLFIFTVVS/LV

<221> polyA_signal

<222> 606..611

<221> polyA_site

<222> 628..639

<400> 276

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atcgaagttt aaagaagggg aaacaggaga cagaaatata ctgaacaaa aagattcaaa 120
agagcaagtg gaatctctaa ga atg gct tcc agc cac tgg aat gaa acc act 172
                                     Met Ala Ser Ser His Trp Asn Glu Thr Thr
                                     -45 -40
acc tct gtt tat cag tac ctt ggt ttt caa gtt caa aaa att tac cct 220
Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro
-35 -30 -25
ttc cat gac aac tgg aac act gcc tgc ttt gtc atc ctg ctt tta ttt 268
Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile Leu Leu Leu Phe
-20 -15 -10
ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc ctt tat gaa gtg 316
Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe Leu Tyr Glu Val
-5 1 5 10
ctt gam wgc tgc tgc tgt gta aaa aac aaa acc gtg aaa gac ttg aaa 364
Leu Xaa Xaa Cys Cys Cys Val Lys Asn Lys Thr Val Lys Asp Leu Lys

```

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          15          20          25
    agt gaa ccc aac cct ctt ara akt atg atg gac aac atc aga aaa cgt      412
    Ser Glu Pro Asn Pro Leu Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg
          30          35          40
    gaa act gaa gtg gtc taacactcta taraaaatga acaaaatctc tgaaagcagc      467
    Glu Thr Glu Val Val
          45
    tcaacctctt ctgaraaaaa aaatatattc tgaggccaac tgttgctaca aaacaaattc      527
    tgactgaatg gttaaaacat ttctagtara aggggaaaaa aaakttaaac atgcactgtt      587
    tgtgtgtata sccatttcat taaatatata gtaaaactyc aaaaaaaaaa aa      639

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<210> 277
 <211> 772
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 284..463
 <221> sig_peptide
 <222> 284..379
 <223> Von Heijne matrix
 score 3.79999995231628
 seq TFINITLWLGS LC/QR

<221> polyA_site
 <222> 762..772

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<400> 277
    acagctgggg ctttgtcttc tttattgcta ggagaatgta gcaatagaag ttctcatcgc      60
    cctgtattgc acttttggtt ttaaggactg gaccagagt tcctgaaagc caaactccat      120
    aagctgctca gtaagttcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct      180
    gttgaatgaa ggtagacgca gcaggcagtt tgctcttacc agtgacctgg aagacgggtgg      240
    cacttcctga gtgagctcac ttaccttccc tgaatggtga ggc atg gat gaa tat      295
                                Met Asp Glu Tyr
                                -30
    tcc tgg tgg tgc cac gtg tta gag gtg gta aag ggt caa atg ttt act      343
    Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly Gln Met Phe Thr
                                -25          -20          -15
    ttt att aat att aca tta tgg ctt ggt tct ctg tgt cag cga ttt ttc      391
    Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys Gln Arg Phe Phe
                                -10          -5          1
    tat gcc tcg ggt act tat ttc cta ata tat atc agc aca gta acg cct      439
    Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro
    5          10          15          20
    agc tgg agg ctt tgt ctt gtt agt tgataaatta gtggtaacag gtagatttgg      493
    Ser Trp Arg Leu Cys Leu Val Ser
          25
    ttacctccca aagtgtggg attrcagacg tgagccaccg cgcttgccg aaacaattct      553
    tttgaaagag agaagtctcc ctgtgttgcg caggctggtc tcagactcct ggggtcaagt      613
    gagcctcctg ctttcgcctc ctaaagtgtc gggattacag gcgtgagcca ccgcacccgg      673
    acagatgtgt tgattttaa gtgggtatga ggcctgagcc ctggagtttg agaccagcct      733
    ggacaacatg gcaagaccct gtctctccaa aaaaaaaaaa      772

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<210> 278
 <211> 840
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 162..671

<221> sig_peptide

<222> 162..398

<223> Von Heijne matrix

score 4.09999990463257

seq QGVLFICFTCARS/FP

<221> polyA_signal

<222> 805..810

<221> polyA_site

<222> 830..840

<400> 278

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ctgcaacgcg cgtgggaggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg      120
atgtttcccg ggaagaactg ggataaaggg gtcccagcac c atg gag gac ccg aac      176
                                   Met Glu Asp Pro Asn
                                   -75

cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc      224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
      -70      -65      -60

cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc      272
Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr
      -55      -50      -45

cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg      320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met
      -40      -35      -30

aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc      368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val
      -25      -20      -15

ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa gcc      416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala
      -10      -5      1      5

ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg      464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu
      10      15      20

ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt      512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
      25      30      35

ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr      560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa Arg His Xaa Gln Xaa
      40      45      50

cat gar gtc cgt gcc cct cct ggc acc ttc gcc tgc aca rad tgc ggt      608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Xaa Cys Gly
      55      60      65      70

cag gac ttt gct car gaa rca ggg ctg cat caa cac tac att cgg cat      656
Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln His Tyr Ile Arg His
      75      80      85

gcc cgg ggg gga ctc tgagttcagc ttaagcctct ccacggtgac ggggtggctct      711
Ala Arg Gly Gly Leu
      90

gtggctggta ggactcacc atgatatggg gtgcaggaac tctggggggc ctgaaggatt      771
tgcttccctc ccctgggaag gcagagggct cttaataaag aggacccaka agattcttaa      831
aaaaaaaaa                                         840

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<210> 279
 <211> 840
 <212> DNA
 <213> Homo sapiens

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 <222> 63..632

<221> sig_peptide
 <222> 63..308
 <223> Von Heijne matrix
 score 4.40000009536743
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 808..813

<221> polyA_site
 <222> 829..840

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 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp
 -80 -75 -70
 ttt cac aga aga tct ctg cca ggc aag gcc atc tta gag att gga gct 155
 Phe His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala
 -65 -60 -55
 gga gtg agc ctt cca gga att ttg gct gcc aaa tgt ggt gca gaa gta 203
 Gly Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val
 -50 -45 -40
 ata ctg tca gac agc tca gaa ctg cct cac tgt ctg gaa gtc tgt cgg 251
 Ile Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg
 -35 -30 -25 -20
 caa agc tgc caa atg aat aac ctg cca cat ctg cag gtg gta gga cta 299
 Gln Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu
 -15 -10 -5
 aca tgg ggt cat ata tct tgg gat ctt ctg gct cta cca cca caa gat 347
 Thr Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp
 1 5 10
 att atc ctt gca tct gat gtg ttc ttt gaa cca gaa rat ttt gaa gac 395
 Ile Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp
 15 20 25
 att ttg gct aca ata tat ttt ttg atg cac aar aat ccc aag gtc caa 443
 Ile Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln
 30 35 40 45
 ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct 491
 Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala
 50 55 60
 tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct 539
 Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser
 65 70 75
 ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga 587
 Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg
 80 85 90
 cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc 632
 His Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105
 tgaattatac ctacaacctg ttctgggaca gtatcaatac tgatgagcaa cctggcacac 692
 aaactatgag cagaccactt cagcttgaga atgcagtggg tctgaagatg gtcaagtctg 752

tttgccttar attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa 812
 aatacgtatt acaagcaaaa aaaaaaaa 840

<210> 280

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..362

<221> sig_peptide

<222> 21..200

<223> Von Heijne matrix

score 4.80000019073486

seq LVILSLKSQTLDA/ET

<221> polyA_signal

<222> 821..826

<221> polyA_site

<222> 838..849

<400> 280

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 Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
 -45 -40 -35
 gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att 149
 Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
 -30 -25 -20
 aaa gaa tgc cat ctc gtc ata ctg tcg ctg aag agc caa acc tta gat 197
 Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
 -15 -10 -5
 gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga 245
 Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
 1 5 10 15
 atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt 293
 Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
 20 25 30
 tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa gac ctg 341
 Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu
 35 40 45
 ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt 392
 Phe Glu Leu Phe Ser Ser Lys
 50
 ggtgggctgg gaactcaatg tcttgtgatc kcccttwgga ttkctctakg ctygckgttg 452
 gaatataacc aattataccw cagctgtaka aatwttgttt taatgtgggg taccygggtg 512
 ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt 572
 catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga 632
 gcttaaagca agtcttcact tgaaaactgc tatagaaatg ctttatattt aaaaatgaaa 692
 gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc 752
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 tcctttataa taaactggta aatgtaaaaa aaaaaaa 849

<400> 281																	
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-105 -100																	
tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca																	101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser																	
-95 -90 -85																	
atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc																	149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg																	
-80 -75 -70																	
aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt																	197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu																	
-65 -60 -55 -50																	
tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct																	245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro																	
-45 -40 -35																	
aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag																	293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln																	
-30 -25 -20																	
gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc																	341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe																	
-15 -10 -5																	
ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg																	389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr																	
1 5 10 15																	
cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa																	437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln																	
20 25 30																	
aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg																	485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu																	
35 40 45																	
gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag																	533
Glu Lys Ser Ile Met Leu																	
50																	
atgatgaccg ttcattaata aatttgcac tcacgacac cagttacttc ctctttgtga																	593
tggtgataac aatgttttgc tatgctgtta tcaagggcag acctagcaaa ttgcgtcaga																	653
gcaatcctga attttgtccc gagaagggtgg ctttggctga agcctaattc cacagctcct																	713
tgttttttga gagagactga gagaaccata atccttgccat gctgaaccca gcctgggcct																	773
ggatgcctcg tgaatacatt atcttgcgat gttggggttat tccagccaaa gacatttcaa																	833
gtgcctgtaa ctgatttga catatttata aaaaatttatt cagaaattgg tccaataatg																	893
cacgtgcttt gccctggta caqccagagc ccttcaaccc caccttggac ttgaaggact																	953

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acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac 1013
gatgttttca ccaaggtcac aggagcattg cgtcgctgat ggggttgaag tttggtttgg 1073
ttcttgtttc agcccaatat gtagagaaca tttgaaacag tctgcacctt tgatacggta 1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgtctgtgg ctttaataatc 1193
atagtaacaa caataatacc tttttctcca ttttgcttgc aggaaacata ccttaagttt 1253
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<210> 282
 <211> 671
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..201

<221> sig_peptide
 <222> 1..63
 <223> Von Heijne matrix
 score 5.09999990463257
 seq LLLKIWLLQRPES/QE

<221> polyA_signal
 <222> 637..642

<221> polyA_site
 <222> 660..671

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-20 -15 -10
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg 96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
-5 1 5 10
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt 144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
15 20 25
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca 192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
30 35 40
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtctttgg 241
Leu Arg Met
45
ctcagttcat ttaaaaaaga tatctatattg aaagttctca rarttgtaca tatgtttcac 301
agtacaggat ctgtacataa aagtttcttt cctaaaccat tcaccaagag ccaatatota 361
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtcttc cttgttattt 421
ctgtttgttaa racttaagtg agttaggtct ttaaggaaag caacgctcct ctgaaatgct 481
tgtctttttt ctgttgccga aatarctggg cctttttcgg gagttaratg tatarartgt 541
ttgtatgtaa acatttcttg taggcattcac catgaacaaa gatataattt ctatttattt 601
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 <212> DNA
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Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu																
-25 -20 -15																
ctc acc agt gcc ctg cac gga ctg cag cag cag cac cca gcc ttc tct	152															
Leu Thr Ser Ala Leu His Gly Leu Gln Gln Gln His Pro Ala Phe Ser																
-10 -5 1 5																
ggg gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt	200															
Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly																
10 15 20																
gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc	248															
Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Leu Phe																
25 30 35																
ctg cac cct gag ccc ttc acc cct ccg agt tcc ccc cag gtt ggc ttc	296															
Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe																
40 45 50																
ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc	344															
Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro																
55 60 65 70																
ctc ttt gtc aac ctg aat aat gag ctg act gtg gag gag cag gtg gar	392															
Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu																
75 80 85																
atc cgc agt ggc ttc ctg gca gct cgg gca cag ctg ccc gtc atg gtc	440															
Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val																
90 95 100																
att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga	488															
Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly																
105 110 115																
ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc	536															
Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa																
120 125 130																
ctg ccc atg tta rar aas cag ctg atg gat ccc cgg gga cct ggg gac	584															
Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp																
135 140 145 150																
atc agg aca gkg ttc cgg ccg ccc ttg gac att tac gac gtg ctg att	632															
Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile																
155 160 165																
cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr	680															
Arg Leu Ser Pro Arg His Ile Pro Arg His Arg Gln Ala Val Asp Ser																
170 175 180																
cca gct gcc tcc ttc tgc cgg ggc ctg ctg agc cag ccg ggg ccc tca	728															
Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu Ser Gln Pro Gly Pro Ser																

```

      185              190              195
tcc ctg atg ccc gtg ctg ggc tak gat cct cct cag ctc tat ctg acg      776
Ser Leu Met Pro Val Leu Gly Xaa Asp Pro Pro Gln Leu Tyr Leu Thr
      200              205              210
cag ctc arg gag gcc ttt ggg gat ctg gcc ctt ttc ttc tat gac cag      824
Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala Leu Phe Phe Tyr Asp Gln
      215              220              225              230
cat ggt gga gag gtg att ggt gtc ctc tgg aag ccc acc agc ttc cag      872
His Gly Gly Glu Val Ile Gly Val Leu Trp Lys Pro Thr Ser Phe Gln
      235              240              245
ccg cag ccc ttc aag gcc tcc agc aca aag ggg cgc atg gtg atg tct      920
Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys Gly Arg Met Val Met Ser
      250              255              260
cga ggt ggg gag cta gta atg gtg ccc aat gtt gaa gca atc ctg gag      968
Arg Gly Gly Glu Leu Val Met Val Pro Asn Val Glu Ala Ile Leu Glu
      265              270              275
gac ttt gct gtg ctg ggt gaa ggc ctg gtg cag act gtg gag gcc cga      1016
Asp Phe Ala Val Leu Gly Glu Gly Leu Val Gln Thr Val Glu Ala Arg
      280              285              290
agt gag agg tgg act gtg tgateccagc tctggagcaa gctgtagacg      1064
Ser Glu Arg Trp Thr Val
      295              300
gacagcagga cattggacct ctagagcaag atgtcagtag gatgacctcc accctccttg      1124
gacatgaatc ctccatggag ggcctgctgg ctgaacatgc tgaatcatct ccaacaaaac      1184
ccagcccaaa ctttctctct gatgtccag cattggggca ggggcatggt ggcccatgta      1244
gtctcctggg cctcaccatc ccagaagagg agtgggagcc agctcagaga aggaactgaa      1304
cccaggagat ccattccact attagccctg ggcctggacc tccctgcgat tccccactcc      1364
ttctcttagtc ttcttcaga aacagagaag gggatgtgtg octgggagag gctctgtctc      1424
cttctgtctg ccaggacctg tgcctagact tagcatgcc ttcactgcag tgtcaggcct      1484
ttagatggga ccagcgaaa atgtggccct tctgagtcac atcaccgaca ctgagcagtg      1544
gaaaggggct atatgtgtat gaatagacca cattgaagga gcaaaaaaaaa aaamcch      1601

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<210> 284
 <211> 1206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..263

<221> sig_peptide
 <222> 69..125
 <223> Von Heijne matrix
 score 3.90000009536743
 seq ALSMSSFSFHSSS/CS

<221> polyA_signal
 <222> 1173..1178

<221> polyA_site
 <222> 1196..1205

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<400> 284
acatttgtga ctttaccaat accctcccag ttcttgatag acagctgtag gttgctgggt      60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt      110
      Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser
      -15              -10
ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc      158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser

```

```

-5          1          5          10
aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta      206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu
          15          20          25
gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa      254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys
          30          35          40
att gtg ggc tgatttggtc ttctctctct cctcccactg ttactgcctt      303
Ile Val Gly
          45
gcagcccttg ttcagggtgta cagaccctta ttctggcctc tagtgctcctt gtctgtcatg      363
acacaccctt ccgccccaaat acctctgacc ccaaggctgg aatggggctg gtaggarata      423
agtttgctta ctcatartca tgtcctttct cttggcacct gcttcctgc ggtgtcctca      483
aatggatttc tgtgtggcag tggartgatt gcatgaattt ttctgtaaca cattaacttt      543
gtattattat taagggartt tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa      603
aactggagcc caaakaaatt cccttagggc aagattatgt tataataraa aattgaattt      663
cctgaggcag tggctgccac cccttttcar atgtttagtc ctgcaaatag catctttctt      723
gtagtctgtg acatggatgg ggatgctagg gcccttaggg gcaaggggac taaactaaat      783
caakttagt ttttttccag caggggttar gggagggtact csctgttgat atttgacact      843
aaaaagtaat cttttttaca aaactgtttt tctagggtgg tggaaagtga aactgccaca      903
tccttggtgg ttttagtcaa raratcattt gcaacaacag taratgtccg ggttttgttt      963
ctgtcctttt attatgaaaa actatgttaa gggggaaaat gtggattatg gtaaccarag      1023
gaatccctas ccttggtttc cttaraarac ttgttttagt ttttatcara cgtctgttgt      1083
agttgtarac aggaaagctt gtgaraaaaa caccacatgg ascctgtaaa tgtttttgca      1143
caacctgtaa agcattcttg gaaktggcca gtaaaaaggg gttttaccat ttaaaaaaaa      1203
aat                                                                1206

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<210> 285

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..285

<221> sig_peptide

<222> 115..204

<223> Von Heijne matrix

score 3.70000004768372

seq SMMLLTVYGGYLC/SV

<221> polyA_signal

<222> 505..510

<221> polyA_site

<222> 525..536

<400> 285

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acgagtgctg cgttcggtg tgctgggaag ttgcgtagac agtggcctcg agaccctgcc      60
tgcctgagga ggcctcggtt ggatgcgaag gagctgcagc atccagggga caag atg      117
                                                                Met
                                                                -30
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc      165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
          -25          -20          -15
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga      213
Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
          -10          -5          1
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa      261

```



```

Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu
   5              10              15
gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tcttgagcar   315
Glu Gln Lys Xaa Ser Gly Ile Met
20              25
asakgccccaa ggcattgctgt ggagagactt cacctgccac catttccagg tcaacaggac   375
tagagcgttg atggttttca aaccctgttg gaagaaagtg cccatgggtt ctctggttct   435
gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca   495
cctacagaca ttaaataatt tgctgtgtca aaaaaaaaaa a                       536

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<210> 286
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..344

<221> sig_peptide
 <222> 90..140
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLITAILAVAVG/FP

<221> polyA_signal
 <222> 500..505

<221> polyA_site
 <222> 515..527

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<400> 286
aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca   60
gagagaaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc   113
                               Met Lys Lys Val Leu Leu Leu Ile
                               -15                               -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag   161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                               -5                               1                               5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr   209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
                               10                               15                               20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att   257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
                               25                               30                               35
cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata   305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile
                               40                               45                               50                               55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa   354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                               60                               65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat   414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta   474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc       529

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<210> 287
 <211> 493
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..311

<221> sig_peptide

<222> 57..107

<223> Von Heijne matrix

score 8.19999980926514

seq LLLITAILAVAVG/FP

<221> polyA_signal

<222> 467..472

<221> polyA_site

<222> 482..493

<400> 287

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aacttgccat ttctcataac agcgtcagag agaaagaact gactgaaacg tttgag atg      59
                                     Met
aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt      107
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
      -15                -10                -5
ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac      155
Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp
1           5           10           15
agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca      203
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
      20           25           30
ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga      251
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
      35           40           45
cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt      299
Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
      50           55           60
ccg agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga      351
Pro Ser Glu Lys
65
aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaa gaaaaacaaa      411
tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa      471
acatgaaagc aaaaaaaaaa aa      493

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<210> 288

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 96..302

<221> sig_peptide

<222> 96..182

<223> Von Heijne matrix

score 5

seq ELSLLPSSLWVLA/TS

<221> polyA_site

<222> 501..514

<400> 288

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aagagacgtc accggctgcg cccttcagta tcgcggacgg aagatggcgt ccgccacccg      60
tctcatccag cggctgcgga actgggcgtc cgggc atg acc tgc agg gga agc      113
                               Met Thr Cys Arg Gly Ser
                               -25
tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca      161
Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
-20                               -15                               -10
agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca      209
Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
-5                               1                               5
ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt      257
Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
10                               15                               20                               25
crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg      302
Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu
30                               35                               40
tagctgccac tgaaaaaraag gcggtgactc cagctcctcc cataaagagg tgggagctgt      362
cctcggacca gccttacctg tgacactgca cctcacggc cacccgacta ctttgctcc      422
ttggatttcc tccagggaga atgtgaccta atttatgaca aatacgtara gctcaggtat      482
cacttctagt ttactttaaa aaaataaaaa aatagagac      521

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<210> 289

<211> 811

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..526

<221> sig_peptide

<222> 161..328

<223> Von Heijne matrix

score 4.19999980926514

seq XSPLLTLALLGQC/SL

<221> polyA_site

<222> 799..811

<400> 289

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aaaaaattgc agtgctgaag aacttgacc cgcaaaaggc tgccctccc aaacctggga      60
ttctgggctc actgagttca cctgcgagtc agccctacct gcactgctct ggtctagtag      120
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc      175
                               Met Val Pro Trp Pro
                               -55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc      223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
-50                               -45                               -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct      271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
-35                               -30                               -25                               -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg      319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
-15                               -10                               -5
ggg cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa      367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
1                               5                               10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg      415

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Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
 15                20                25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa    463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
 30                35                40                45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt    511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
                50                55                60
caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaas cttcaaara    566
Gln Phe Phe Leu Gly
                65
caatgttatt acagcaktct ccccttatcc aaaktttcct tttcctgadt ttcagttagc    626
tatggccaac cgcttggaac atakttgaac acagtacaat aaratatattt gaggttgga    686
ktgggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact    746
tgaacccagg aktttgarac caccctgggc aacatrgtra gacctcatct ctacaaaaaa    806
aaaaa                                           811

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<210> 290
 <211> 625
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 210..332

<221> sig_peptide
 <222> 210..299
 <223> Von Heijne matrix
 score 8.10000038146973
 seq ITCLLAFWVPASC/IQ

<221> polyA_signal
 <222> 594..599

<221> polyA_site
 <222> 613..625

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<400> 290
acaggtcsmc ttaacatctc ttgatttgag ccactccac tgtcatcagc tttcacctgg    60
attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttcctaataa    120
atgcattgca tagttgatca agtcactctc tggcctaata ccttccttgg ctccctgctg    180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc    233
                                Met Ala Cys Glu Thr His Gly Val
                                -30                -25
ctt gtc cct gct cac ctc tct ggt ctc atc act tgc ctt ctt gca ttc    281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
                -20                -15                -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca    329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
                -5                1                5                10
ctc tgattcctcc tttcttttgg tcacagagaa agggactttt ctctgtcaaa    382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc    442
accctggcat actacacara tcactctggg ctcaactggc tgcctaattg tcatctcccc    502
agtaaactgt aagctccttg agggcaagga ttgtgttggg atttttgtat taacagtgcc    562
tggcttggtg cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaa    622
aaa                                           625

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<210> 291
 <211> 684
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 212..361

<221> sig_peptide
 <222> 212..319
 <223> Von Heijne matrix
 score 4.09999990463257
 seq HWLFLASLSGIKT/YQ

<221> polyA_signal
 <222> 650..655

<221> polyA_site
 <222> 673..684

<400> 291
 atccccawns cactctctca cagagactgt tcttttctct ctgagaccct actccagctt 60
 gtagttctaa atctgtgatt atgcactgtc tgtcttcttc ttgaggtcag gggccatttc 120
 ttttggtctc tgctatgctc aggaccaga tcaaaggagc tcagtaacta ttacagggcg 180
 tacatcatat gtggaggaca cttatgctgt g atg gcc cca cac aca gct tcc 232
 Met Ala Pro His Thr Ala Ser
 -35 -30
 ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc gtg gta gcc act gag 280
 Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu
 -25 -20 -15
 cac tgg ctc ttc ctg gct tca ctc tct ggc atc aaa act tat cag tcc 328
 His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser
 -10 -5 1
 tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattaccta attcacacra 381
 Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile
 5 10
 aggtgttaat ggtggtaatg gcataktatt tattacccca ggggaccak aacggtggta 441
 tcaaaacata tcattcccca gtggtttaaa actctggtag ctttccargg aatccaaagt 501
 ggaatccagt ctccttagct gawttcacag ggccccgtct gcacaacttg gcttctgtcg 561
 gcttccttan ccctgacttc ccaagcctta gtcacaccc tctctccac ccagggctca 621
 gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcac yaaaaaaaaa 681
 aaa 684

<210> 292
 <211> 628
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..482

<221> sig_peptide
 <222> 75..128
 <223> Von Heijne matrix
 score 3.59999990463257
 seq KMLISVAMLGAXA/GV

<221> polyA_signal

<222> 595..600

<221> polyA_site

<222> 618..627

<400> 292

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aagtgagacc gcgcggcaac agcttgccgc tcgsgggagc tcccgaggc gctccgctgg      60
ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca      110
              Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
              -15                      -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg      158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
      -5              1              5              10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg      206
Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
              15              20              25
cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg      254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
              30              35              40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg      302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
              45              50              55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac      350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His
              60              65              70
cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc      398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
              75              80              85              90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg      446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
              95              100              105
amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg      492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
              110              115
tcgggtgagc acgtgtcccc caaacctgg actgactgct ttaagggtccg caaggcgggc      552
cagggccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcctc      612
cammcaaaaa aaaaah      628

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<210> 293

<211> 813

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 50..631

<221> sig_peptide

<222> 50..244

<223> Von Heijne matrix

score 8

seq LTLIGCLVTGVES/KI

<221> polyA_signal

<222> 777..782

<221> polyA_site

<222> 801..812

<400> 293

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aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                     Met Gln Asp
                                     -65
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
      -60      -55      -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
      -45      -40      -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
      -30      -25      -20      -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
      -10      -5      1
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac      298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
      5      10      15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
      20      25      30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
      35      40      45      50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg
      55      60      65
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg      490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu
      70      75      80
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt      538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val
      85      90      95
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt      586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys
      100      105      110
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc      631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser
      115      120      125
taaactggaa ctggaccag gatgctttgc ascaacgccc tagggtttgc agtgaatgtc      691
caaatgcttg tgatcatcttg tccggtttcc tcccaatatt ccttctcaaa cttggagagg      751
gaaaattaag ctatactttt aagaaaaataa atatttccat ttaaatgtca amaaaaaaaaa      811
ah                                                    813

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<210> 294

<211> 778

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..576

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix
 score 4.80000019073486
 seq MMVLSLGIILASA/SF

<221> polyA_signal

<222> 737..742

<221> polyA_site

<222> 763..775

<400> 294

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agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga      60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag      120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc      174
                               Met Thr Ser Gln Pro Val Pro
                               -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
      -60                               -55                               -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
      -45                               -40                               -35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt      318
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
      -30                               -25                               -20                               -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
      -10                               -5                               1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
      5                               10                               15
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg      462
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg
      20                               25                               30
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct      510
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa
      35                               40                               45                               50
gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa      558
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu
      55                               60                               65
tct tgt tct cct gtc ggg targataaca ggggttgctt ratttttagat      606
Ser Cys Ser Pro Val Gly
      70
caatttctta tcagactcaa ataaacattt cttttgaaaa tcattcttatt cttcacatta      666
tcattcttgag ctatgatgga aactagtgas ktctctccag gtttaggcga aaaaaaaatc      726
catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaaah cc      778

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<210> 295

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..897

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix

score 4.80000019073486

seq MMVLSLGIILASA/SF

<221> polyA_signal

<222> 1017..1022

<221> polyA_site

<222> 1044..1054

<400> 295

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agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga      60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag      120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc      174
                               Met Thr Ser Gln Pro Val Pro
                               -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
                               -60                               -55                               -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
                               -45                               -40                               -35
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt      318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
                               -30                               -25                               -20                               -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
                               -10                               -5                               1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
                               5                               10                               15
cca ttc ata gga ccc ttt ttt ttt atc atc tct ggc tct cta tca atc      462
Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
                               20                               25                               30
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt      510
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val
                               35                               40                               45                               50
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg      558
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu
                               55                               60                               65
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg      606
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu
                               70                               75                               80
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat      654
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His
                               85                               90                               95
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct      702
Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala
                               100                               105                               110
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa      750
Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa
                               115                               120                               125                               130
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc      798
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe
                               135                               140                               145
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm      846
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly
                               150                               155                               160
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act      894
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr
                               165                               170                               175
tct taagaaaaaa gggagaaata ttaatcagaa agttgattct tatgataata      947
Ser
tgaaaaagtt aaccattata gaaaagcaaa gcttgagttt cctaaatgta agctttttaa      1007
gtaatgaaca ttaaaaaaaa ccattatttc actgtcaaaa aaaaaamcc nkt      1060

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<210> 296
 <211> 444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 146..292

<221> sig_peptide
 <222> 146..253
 <223> Von Heijne matrix
 score 5.5
 seq FTSMCILFHCLLS/FQ

<221> polyA_signal
 <222> 395..400

<221> polyA_site
 <222> 433..444

<400> 296
 aacttgggac aagaratcaa acttttaaaga tgggtctaaag cccctcttaa aggtctgact 60
 gtgtcggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc 120
 ctttcatttc attctagaag acccc atg caa gtt ccc cac cta agg gtc tgg 172
 Met Gln Val Pro His Leu Arg Val Trp
 -35 -30
 aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca 220
 Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg. Asn Leu Gly Phe Thr
 -25 -20 -15
 agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa 268
 Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
 -10 -5 1 5
 aag aaa aga aaa ctt ara ctt ttc tgatgttctt ttttacgtaa ataaccattt 322
 Lys Lys Arg Lys Leu Xaa Leu Phe
 10
 tattgttggt ttgctttttc tgccttcaaa ctactccac aggccaaata tavctggctg 382
 cttctttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa 442
 aa 444

<210> 297
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..383

<221> sig_peptide
 <222> 126..167
 <223> Von Heijne matrix
 score 7.5
 seq VALNLILVPCCAA/WC

<221> polyA_signal
 <222> 726..731

<221> polyA_site
 <222> 743..754

<400> 297

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aattgtatgt tacgatgttg tattgatttt taagaaagta attkratttg taaaacttct      60
gctcgtttac actgcacatt gaatacaggt aactaattgg wggagaggg gaggtcactc      120
ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg      170
    Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
          -10          -5          1
tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct      218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser
          5          10          15
gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt      266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly
          20          25          30
tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga      314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg
          35          40          45
ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag      362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu
          50          55          60          65
gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar      413
Gly His Arg Ile Cys Asp Leu
          70
aaaccacagt cttcccagca attattacaa ttcttgaatt ccttggggat tttttactgc      473
cctttc aaag cacttaaktg tkrratctaa cgkttccag tgtctgtctg aggtgactta      533
aaaaatcaga acaaaacttc tattatccag agtcattgga gagtacaccc tttccaggaa      593
taatgttttg ggaaacactg aaatgaaatc ttcccagtat tataaattgt gtatttaaaa      653
aaaagaaact tttctgaatg cctacctggc ggtgtatacc aggcagtgtg ccagtttaaa      713
aagatgaaaa agaataaaaa cttttgagga aaaaaaaaaa a                        754

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<210> 298

<211> 629

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 66..497

<221> sig_peptide

<222> 66..239

<223> Von Heijne matrix

score 5.40000009536743

seq QLLDSVLWLALG/LT

<221> polyA_signal

<222> 594..599

<221> polyA_site

<222> 618..629

<400> 298

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aactcccaga atgctgacca aagtgggagg agcactaggt cttcccgta cctccacetc      60
tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg      110
    Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro
          -55          -50          -45
atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt      158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser
          -40          -35          -30
cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc      206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu

```

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      -25      -20      -15
ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca 254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala
      -10      -5      1      5
gtc ttt tcc acc act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc 302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe
      10      15      20
ctc acc ttt gac ctg ctc cat agg ccc gca gtc aca ctc tgc cac agc 350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser
      25      30      35
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg 398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu
      40      45      50
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac 446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn
      55      60      65
tta gcc tcc agg aag cac tgc tgc tgc tgc tca tgg ggc tgg gcc cgc 494
Leu Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg
      70      75      80      85
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct 547
Ser -
ccatccttgg gcctgakanc ccttccccac aactcagtgt cttcaaata tacaatgacc 607
acccttcttc aaaaaaaaaa aa 629

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<210> 299
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..411

<221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix
 score 10.1000003814697
 seq LVLTLCPLAVA/SA

<221> polyA_signal
 <222> 732..737

<221> polyA_site
 <222> 750..763

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<400> 299
aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgctc atg gag agg 57
                                         Met Glu Arg
                                         -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
      20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc 249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro

```

```

      40      45      50
ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg 297
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro
      55      60      65
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc 345
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly
      70      75      80
cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tcg 393
Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser
      85      90      95
ggc gag cat ccs rva btg tgaatkkkga cttttttctc ckccatttga 441
Gly Glu His Pro Xaa Xaa
100      105
agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tcaactgaatt tacaaaraca 501
gcaggaacrs ackggtgggg atgggcagct gttcrargcr atggggtkac tgcccttcct 561
ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggaatcgat 621
acagtgtatg acaatgtcat atagtataac acaacataat gaataatacg tgtatattgc 681
aacttaatat aatacgatgt aatataatgc tacataatac aacataatat aataaaatag 741
aatgcaacac aaaaaaaaaa aacc 765

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<210> 300
 <211> 623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..534

<221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix
 score 10.1000003814697
 seq LVLTLCTLPLAVA/SA

<221> polyA_signal
 <222> 593..598

<221> polyA_site
 <222> 612..623

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<400> 300
aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgctc atg gag agg 57
                                   Met Glu Arg
                                   -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
      40      45      50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
      55      60      65

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atg aak ttc gaa tgg tgc ccg gcc ccc atg gtg caa ggc gtg atc acc      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
      70                      75                      80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
      85                      90                      95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tgc      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
      100                    105                    110                    115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
      120                    125                    130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
      135                    140                    145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa      594
taaactctca tgcccccaaa aaaaaaaaaa      623

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<210> 301
 <211> 571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..415

<221> sig_peptide
 <222> 86..145
 <223> Von Heijne matrix
 score 9.80000019073486
 seq FTIGLTLLLGXQA/MP

<221> polyA_signal
 <222> 540..545

<221> polyA_site
 <222> 560..571

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<400> 301
aaaaactcac ccagtgagtg tgagcattta agaagcatcc tctgccaaga ccaaaaggaa      60
agaagaaaaaa bggccaaaag ccaaaa atg ara ctg atg gta ctt gtt ttc acc      112
Met Xaa Leu Met Val Leu Val Phe Thr
      -20                      -15
att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc      160
Ile Gly Leu Thr Leu Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg
      -10                    -5                      1                      5
ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt      208
Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu
      10                      15                      20
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat      256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp
      25                      30                      35
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc      304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe
      40                      45                      50
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat      352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp
      55                      60                      65
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct      400

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Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser
 70 75 80 85
 ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt 455
 Gly Glu His His Ser
 90
 tctagtttct atatagtgca atagagcata gattctataa attcttactt gtctaagaaa 515
 gtaaactctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaa 571

<210> 302
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..268

<221> sig_peptide
 <222> 56..100
 <223> Von Heijne matrix
 score 4.59999990463257
 seq LLTHNLLSSHVRG/VG

<221> polyA_signal
 <222> 584..589

<221> polyA_site
 <222> 601..612

<400> 302
 ctaatcgaaa aggggggattt tccgggtccg gcctggcgag agtttgtgcy gcgac atg 58
 Met
 -15
 aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg 106
 Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
 -10 -5 1
 tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc 154
 Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
 5 10 15
 cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg 202
 Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val
 20 25 30
 gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag 250
 Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln
 35 40 45 50
 gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagtttct 298
 Val Pro Arg Arg Ala Gly
 55
 gaggaccatg caccacctgc tgctggaggt ggamstgaka gagggcaccc tgcagtgcc 358
 ggaatctgga cgtatgttcc ccatacagccg cgggatcccc aacatgctgc tgagtgaaga 418
 ggaaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg 478
 ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac 538
 accaaacaca gtgtttttga gctcgggtatt atatattttt ttctcattaa aggtttaaaa 598
 ccaaaaaaaaa aaaa 612

<210> 303
 <211> 539
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..328

<221> sig_peptide

<222> 32..103

<223> Von Heijne matrix

score 4.59999990463257

seq FFIFCSLNTLLLG/GV

<221> polyA_signal

<222> 508..513

<221> polyA_site

<222> 528..539

<400> 303

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aacaactatc ctgctgctg cttgctgcac c atg aag tct gcc aag ctg gga      52
                                   Met Lys Ser Ala Lys Leu Gly
                                   -20
ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg      100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
      -15                                -10                                -5
ggg ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat      148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp
      1                                5                                10                                15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt      196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
      20                                25                                30
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc      244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
      35                                40                                45
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt      292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg
      50                                55                                60
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg      338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg
      65                                70                                75
tgaactcatg aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcaractg      398
atttwgaaat ctttgttwta tttccmymak ggcgwктаag cttccatattg tttgctatgt      458
tcctgacct agttttgtct ttcctggaaa ttaactgtat gacattasa atgaaagagt      518
ctttctgtca aaaaaaaaaa a                                     539

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<210> 304

<211> 964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..527

<221> sig_peptide

<222> 21..95

<223> Von Heijne matrix

score 8.5

seq LKVLLLPLAPAAA/QD

<221> polyA_signal

<222> 921..926

<221> polyA_site

<222> 953..963

<400> 304

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agggcgatc ttctccggcc atg agg aag cca gcc gct ggc ttc ctt ccc tca      53
                Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
                -25                -20                -15
ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat      101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
                -10                -5                1
tcg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac      149
Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr
                5                10                15
caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc      197
Gln Arg Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr
                20                25                30
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag      245
Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln
                35                40                45                50
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc      293
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys
                55                60                65
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act      341
Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr
                70                75                80
cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt      389
His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys
                85                90                95
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa      437
Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu
                100                105                110
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc      485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr
                115                120                125                130
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc      527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala
                135                140
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgtccc tgggaggcca      587
ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca      647
agaacacaag caggaagagg ggcagaaaca ggaagagcaa gaagaggaac aggaagagga      707
gggaaagcag gaagaaggac aggggactaa ggagggaagg gaggtgtgt ctcagctgca      767
gacagactca gagcccaagt ttactctga atctctatct tctaaccctt cctcttttgc      827
tccccgggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat      887
tcgatcagcc caggaaatag atgaaatgaa tgaaatatat gatgagaact cctactggag      947
aaacaaaaaa aaaaaak      964

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<210> 305

<211> 684

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 147..647

<221> sig_peptide

<222> 147..374

<223> Von Heijne matrix
score 3.5
seq LASASELPLGSRP/AP

<221> polyA_site
<222> 668..681

<400> 305
aacttcctgt gagcccgccg gtgacaacgg caacatggcc cgtgaacgga gctgaagtcg 60
acgactcttc ctrgrarmcc ccgactgagg cggagacgaa ggtgctgcag gcgcgacggg 120
agcggcaaga tcgcatctcc cggctc atg ggc gac tat ctg ctg cgc ggt tac 173
Met Gly Asp Tyr Leu Leu Arg Gly Tyr
-75 -70
cgc atg ctg ggc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa 221
Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln
-65 -60 -55
gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca 269
Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser
-50 -45 -40
gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc 317
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser
-35 -30 -25 -20
caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc 365
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly
-15 -10 -5
tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag 413
Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu
1 5 10
gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct 461
Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala
15 20 25
gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg 509
Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu
30 35 40 45
caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg 557
Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa
50 55 60
gga aaa mta gca tcc agc tgt gtg gcc tta tcc gcg cat gtg cgg agg 605
Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg
65 70 75
ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc 647
Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro
80 85 90
tgagaaaaac ctctagaaaa acaaaaaaaaaaaa aaaaccc 684

<210> 306
<211> 693
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 262..471

<221> sig_peptide
<222> 262..306
<223> Von Heijne matrix
score 3.5
seq LCFLLPHHRLQEA/RQ

<221> polyA_signal

<222> 663..668

<221> polyA_site

<222> 682..693

<400> 306

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atttcgcggc gctcgcgbgma cyhsgwtgtt cagcaccttc ggtccggttg aggttggtcaa      60
gtcggmccaa acaggttggtt tctctgcagt ttccaacatg gcagggmsgt ttaatagaca      120
tggaataaaa gtccactcac agaaatcctg aagatgccag ggctggcaaa tatgaaggta      180
aacacaaacg aaagaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat      240
cagtgcagtc tttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat      291
                        Met Ile Leu Cys Phe Leu Leu Pro His His
                        -15                      -10

cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg      339
Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro Arg
-5                      1                      5                      10
gaa aaa tta aga aga aga gaa gag aga aaa caa ata aat ggg aaa aaa      387
Glu Lys Leu Arg Arg Arg Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys
                      15                      20                      25
raa agg aca aaa tat gaa aca cca aga aaa rga raa gga aaa aaa gga      435
Xaa Arg Thr Lys Tyr Glu Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly
                      30                      35                      40
gga aac mac cmc wtw tkt cmc ctt tcc aar agg gac tgaaactggg      481
Gly Asn Xaa Xaa Xaa Xaa Leu Ser Lys Arg Asp
                      45                      50                      55
ctgacccttt tgatttccaa vctcascgtt ttggtgtaag gcggccaaar aaggatgcgg      541
ascccagcac tgtgaagcct acaaaaaacat tgatgcgctg gcttggggat ttgaatttga      601
acatctttca cactaagttc agactcatga aaccaatctt cagatgctct gtaaaccaca      661
taataaagag tttggaaatt aaaaaaaaaa aa      693

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<210> 307

<211> 1656

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..1216

<221> sig_peptide

<222> 74..172

<223> Von Heijne matrix

score 5.80000019073486

seq XLCLGMALCPRQA/TR

<221> polyA_signal

<222> 1627..1632

<221> polyA_site

<222> 1640..1652

<400> 307

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atctcttggc gtctcaacgt tcggatcagc agcttttttc cattctctct ctccacttct      60
tcagtgcagca gcc atg agt tgg act gtg cct gtt gtg cgg gcc agc cag      109
                        Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln
                        -30                      -25

aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg      157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu
-20                      -15                      -10

```

tgt ccg cgt caa gca acg cgc atc ccg ctc aac ggc acc tgg ctc ttc	205
Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe	
-5 1 5 10	
acc ccc gtg agc aag atg gcg act gtg aar agt gag ctt att gag cgt	253
Thr Pro Val Ser Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg	
15 20 25	
ttc act tcc gar aag ccc gtt cat cac agt aag gtc tcc atc ata gga	301
Phe Thr Ser Glu Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly	
30 35 40	
act gga tcg gtg ggc atg gcc tgc gct atc agc atc tta tta aaa ggc	349
Thr Gly Ser Val Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly	
45 50 55	
ttg agt gat gaa ctt gcc ctt gtg gat ctt gat gaa rac aaa ctg aag	397
Leu Ser Asp Glu Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys	
60 65 70 75	
ggg gag acr atg gat ctt caa cat ggc agc cct ttc acg aaa atg cca	445
Gly Glu Thr Met Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro	
80 85 90	
aat att gtt tgt agc aaa rat tac ttt gtc aca gca aac tcc aac cta	493
Asn Ile Val Cys Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu	
95 100 105	
gtg att atc aca gca ggt gca cgc caa raa aag gga gaa acg cgc ctt	541
Val Ile Ile Thr Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu	
110 115 120	
aat tta stc cag cga aat gtg gcc atc ttc aag tta atg att tcc agt	589
Asn Leu Xaa Gln Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser	
125 130 135	
att gtc cag tac agc ccc cac tgc aaa ctg att att gtt tcc aat cca	637
Ile Val Gln Tyr Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro	
140 145 150 155	
gtg gat atc tta act tat gta gct tgg aag ttg agt gca ttt ccc aaa	685
Val Asp Ile Leu Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys	
160 165 170	
aac cgt att att gga agc ggc tgt aat ctg ata mhg gct cgt ttt cgt	733
Asn Arg Ile Ile Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg	
175 180 185	
ttc ttg att gga caa aag ctt ggt atc cat tct gaa agc tgc cat gga	781
Phe Leu Ile Gly Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly	
190 195 200	
tgg atc ctc gga gag cat gga gac tca agt gtt cct gtg tgg agt gga	829
Trp Ile Leu Gly Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly	
205 210 215	
gtg aac ata gct ggt gtc cct ttg aag gat ctg aac tct gat ata gga	877
Val Asn Ile Ala Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly	
220 225 230 235	
act gat aaa gat cct gag caa tgg aaa aat gtc cac aaa gaa gtg act	925
Thr Asp Lys Asp Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr	
240 245 250	
gca act gcc tat gag att att aaa atg aaa ggt tat act tct tgg gcc	973
Ala Thr Ala Tyr Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala	
255 260 265	
att ggc cta tct gtg gcc gat tta aca gaa agt att ttg aag aat ctt	1021
Ile Gly Leu Ser Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu	
270 275 280	
agg aga ata cat cca gtt tcc acc ata act aag ggc ctc tat gga ata	1069
Arg Arg Ile His Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile	
285 290 295	
rat gaa gaa gta ttc ctc agt att cct tgt atc ctg gga gag aac ggt	1117
Xaa Glu Glu Val Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly	
300 305 310 315	
att acc aac ctt ata aag ata aag ctg acc cct gaa gaa gag gcc cat	1165
Ile Thr Asn Leu Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His	

	320	325	330	
ctg aaa aaa agt gca aaa aca ctc tgg gaa att cag aat aag ctt aag				1213
Leu Lys Lys Ser Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys				
	335	340	345	
ctt taaagttgcc taaaactacc attccgaaat tattgaagag atcatagata				1266
Leu				
caggattata taacgaaatt ttgaataaac ttgaattcct aaaagatgga aacaggaaag				1326
taggtagagt gattttccta tttatttagt cctccagctc ttttattgag catccacgtg				1386
ctggacgata cttattttaca attcckaagt atttttggtg cctctgatgt agcagcactt				1446
gccatgttat atatatgtag ttgrmatttg gttcccaaaa agtaggatgt aggtatttat				1506
tgtgttctag aaattccgac tcttttcatt agatatatgc tatttctttc attcttgctg				1566
gtttatacct atgttcattt atatgctgta aaaaagtagt agcttcttct acaatgtaaa				1626
aataaatgta catacaaaaa aaaaaamcmc				1656

<210> 308
 <211> 517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..164

<221> sig_peptide
 <222> 48..89
 <223> Von Heijne matrix
 score 4
 seq YYMVCLFFRLIFS/EH

<221> polyA_signal
 <222> 482..487

<221> polyA_site
 <222> 505..517

<400> 308	
aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac	56
	Met Tyr Tyr
atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att	104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile	
-10 -5 1 5	
ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca	152
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro	
10 15 20	
aca tct gct ggc taaataaaga catgatcttc accttttggg attgttaatt	204
Thr Ser Ala Gly	
25	
taaaatgggt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctggtg	264
atttatatgg ctcttcacaa ggtgttattt tggggatatca aggtatggat gcttaaatca	324
gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaaa atcaaccttg	384
gtccttccac caaaacccat taatttccat atcatcatct gcataararg gaaaattcct	444
acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg	504
aaaaaaaaaa aaa	517

<210> 309
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..334

<221> sig_peptide
 <222> 185..295
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSYASSALSPCLT/AP

<221> polyA_signal
 <222> 355..360

<221> polyA_site
 <222> 392..405

<400> 309
 atcacattct tctccatcct tstctgggcc agtccccarc ccagtccttc tcttgacctg 60
 cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggccctacct 120
 ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
 tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
 -35 -30 -25
 aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
 Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
 -20 -15 -10
 ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg 325
 Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met
 -5 1 5 10
 cct gac aac taaatattcct tatccaaatc aataaarwra raatcctccc 374
 Pro Asp Asn
 tccaraaggg tttctaaaaa caaaaaaaaa a 405

<210> 310
 <211> 1087
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 195..347

<221> sig_peptide
 <222> 195..272
 <223> Von Heijne matrix
 score 7.09999990463257
 seq LASLQWSLT LAWG/GS

<221> polyA_signal
 <222> 1037..1042

<221> polyA_site
 <222> 1071..1082

<400> 310
 aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt 60
 acctacctta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg 120
 gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgacct agttgctggc 180
 ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg 230

	Met	Thr	Pro	Trp	Cys	Leu	Ala	Cys	Leu	Gly	Arg	Arg	
	-25						-20					-15	
cct ctc gct tct ttg cag tgg agc ctg aca ctg gcg tgg tgt ggc tcc													278
Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser													
	-10						-5					1	
ggc agc cac tgg aca gag aga cca akt cag akt tca ccg tgg akt tct													326
Gly Ser His Trp Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser													
	5						10					15	
ctg tca gcg acc acc agg ggg tgatcacacg gaaggtgaac atccaggtcg													377
Leu Ser Ala Thr Thr Arg Gly													
	20						25						
gggatgtgaa tgacaacgcg cccacatttc acaatcagcc ctacagcgtc cgcattccctg													437
araatacacc agtggggacg cccatcttca tcgtgaatgc cacagacccc gacttggggg													497
cagggggcag cgtcctctac tccttccagc cccctcccca attcttcgcc attgacagcg													557
cccgcggtat cktcacagtg atccggggagc tggactacga taccacrcmg gcctaccagc													617
tcwcggtcwa cgccacagat caagacaara ccaggcctct gtccaccstg gccaacttgg													677
ccatcatcat cacagatgtc caggacatgg accccatctt catcaacctg ccttacagca													737
ccaacatcta cgagcattct cctccgggca cgacgggtgcg catcatcacc gccatagacc													797
aggataaagg acgtccccgg ggcatctggc acaccatcgt ttcaggggcat ctgtgtttac													857
aagaacccaa gatctctcag gagctcagga aaaggggctt gctgtgaggc tcagggttcc													917
catggacatt ctgagctgac cctcctcagc attggatctc ctggctcagg aactaggaac													977
gaagcttga tggtttctcc tttcctacag catctgtatt catttcctat agttgccata													1037
ataaaatgcc actaacttag tggcttaaaa accaaaaaaa aaaaaccctt													1087

<210> 311

<211> 916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 90..815

<221> sig_peptide

<222> 90..179

<223> Von Heijne matrix

score 13.1999998092651

seq LLLLSTLVIPSAA/AP

<221> polyA_signal

<222> 883..888

<221> polyA_site

<222> 905..916

<400> 311

aaaacagtac gtggggcgcc ggaatccggg agtccgggtga cccgggctgt ggtctagcat	60
aaaggcggag ccagaagaag gggcgggggt atg gga gaa gcc tcc cca cct gcc	113
	Met Gly Glu Ala Ser Pro Pro Ala
	-30 -25
ccc gca agg cgg cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg	161
Pro Ala Arg Arg His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu	
	-20 -15 -10
gtg atc ccc tcc gct gca gct cct atc cat gat gct gac gcc caa gag	209
Val Ile Pro Ser Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu	
	-5 1 5 10
agc tcc ttg ggt ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc	257
Ser Ser Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser	
	15 20 25
cga ctt ttc ctg aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc	305

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Arg Leu Phe Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe
      30                      35                      40
tct gcc ccc atg gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag      353
Ser Ala Pro Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu
      45                      50                      55
gag aac cag gag cac cag ctg ggg aac aac acc ctc tcc agc cac ctc      401
Glu Asn Gln Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu
      60                      65                      70
cag atc gac aag atg acc gac aac aag aca gga gag gtg ctg atc tcc      449
Gln Ile Asp Lys Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser
      75                      80                      85                      90
gag aat gtg gtg gca tcc att caa cca vcg gag ggg anc ttc gag ggt      497
Glu Asn Val Val Ala Ser Ile Gln Pro Xaa Glu Gly Xaa Phe Glu Gly
      95                      100                      105
gat ttg aag gth ccc agg atg gag gar aag gag gcc ctg gta ccc mtc      545
Asp Leu Lys Val Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Xaa
      110                      115                      120
car aag gcc acg gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc      593
Gln Lys Ala Thr Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala
      125                      130                      135
ttc tgg atc att aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg      641
Phe Trp Ile Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu
      140                      145                      150
gag ggc ggc cac tgg ctc anc gar aag cga cac cgc ctg cag gcc atc      689
Glu Gly Gly His Trp Leu Xaa Glu Lys Arg His Arg Leu Gln Ala Ile
      155                      160                      165                      170
cgg gat gga ctc cgc aag ggg acc cac aag gac rtc cta daa rag ggg      737
Arg Asp Gly Leu Arg Lys Gly Thr His Lys Asp Xaa Leu Xaa Xaa Gly
      175                      180                      185
acc gar agc tcc tcc cac tcc agg ctg tcc ccc cga aar amm cac tta      785
Thr Glu Ser Ser Ser His Ser Arg Leu Ser Pro Arg Lys Xaa His Leu
      190                      195                      200
ctg tac atc ctc arg ccc tct cgg cag ctg targgggtggg gaccggggar      835
Leu Tyr Ile Leu Xaa Pro Ser Arg Gln Leu
      205                      210
macctgcctg tagcccccat caraccctgc cccaagcacc atatggaaat aaagttcttt      895
cttacatcca aaaaaaaaaa a                                          916

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<210> 312

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..513

<221> sig_peptide

<222> 52..231

<223> Von Heijne matrix

score 4

seq LVRRTLLVAALRA/WM

<221> polyA_signal

<222> 553..558

<221> polyA_site

<222> 572..583

<400> 312


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aaggaaacag caaccagagg gagatgatca cctgaaccac tgctccaaac c atg ggc      57
                                     Met Gly
                                     -60
agt aaa tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag      105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln
                                     -55
                                     -50
                                     -45
agg cgg cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg      153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val
                                     -40
                                     -35
                                     -30
aar gca gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc      201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg
                                     -25
                                     -20
                                     -15
agg acc ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg      249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp
                                     -10
                                     -5
                                     1
                                     5
tgg agg acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg      297
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu
                                     10
                                     15
                                     20
ttr ggg gtc tac gtc atc cag gag cag gcg gcg gtc aag ctc cag tcc      345
Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu Gln Ser
                                     25
                                     30
                                     35
tgc atc cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat      393
Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn
                                     40
                                     45
                                     50
gct ctc tgc ttg ttc cag gtc cca aaa agc agc ctt gcc ttc caa act      441
Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe Gln Thr
                                     55
                                     60
                                     65
                                     70
gat ggc ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag      489
Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu
                                     75
                                     80
                                     85
ttc cac att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg      543
Phe His Ile Glu Ile Leu Ser Ile
                                     90
cactacccta ataaatgtct gaccaggtaa aaaaaaaaaa      583

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<210> 313
 <211> 697
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..438

<221> sig_peptide
 <222> 172..354
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LLPCNLHCSWLHS/SP

<221> polyA_signal
 <222> 682..687

<221> polyA_site
 <222> 685..697

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<400> 313
agattggctg ggcagatggg ctgactggct gggcagatgg gtgggtgagt tccctctccc      60
cagagccatc ggccaggtac caaagctcag ctgtatggat tcccaacagg aggacctgcg      120
cttccttggg acccattgtt gtactggatt aacaagcgac ggcgctacgg c atg aat      177

```


	20	25	30	
gct ggg cgg tgt aag tct ggc ttt gac ctc gac atg gat cac aca ata				366
Ala Gly Arg Cys Lys Ser Gly Phe Asp Leu Asp Met Asp His Thr Ile				
	35	40	45	
taaaaaaaaa aacctggtac ctcattgcac tgtkacttaa attasccttc tgcctcgcac				426
tctgtgctaa actggaacag ttactacca tgaatctatc ctatgtcttc attcctttat				486
gggccttgct ggctggggct ttaacagaac tcggatataa tgtctttttt gtgaaagact				546
gacttctaag tacatcatct cctttctatt gctgttcaac aagttaccat taaagtgttc				606
tgaatctgtc aagcttcaag aataccagag aactgaggga aaataccaaa tgtagtttta				666
tactacttcc ataaaacagg attggtgaat cacggacttc tagtcaacct acagcttaat				726
tattcagcat ttgagttatt gaaatcctta ttatctctat gttaaataaag tttgttttgg				786
acctcaaaaa aaaaaaa				803

<210> 315

<211> 823

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 175..336

<221> sig_peptide

<222> 175..276

<223> Von Heijne matrix

score 3.70000004768372

seq SVLNVGHLLFSSA/CS

<221> polyA_site

<222> 812..823

<400> 315

aaggcgcgcg cgaccggcgg ctctttggcg cggattaggg ggtctcggcg agggagtcac	60
caagcttttg tgatgtgtt ggccggttct gaagtcttga agaagctctg ctgaggaaga	120
ccaaagcagc actcgttgcc aattagggaa tggaccgttt gggttccttt agca atg	177
	Met
atc cct ctg ata agc cac ctt gcc gag gct gct cct cct acc tca tgg	225
Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser Trp	
	-30 -25 -20
agc ctt ata tca agt gtg ctg aat gtg ggc cac ctc ctt ttt tcc tct	273
Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser Ser	
	-15 -10 -5
gct tgc agt gtt tca ctc gag gct ttg agt aca aga aac atc aaa gcg	321
Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys Ala	
	1 5 10 15
atc ata ctt atg aaa taatggcttc agattttcct gtccttgatc ccagctggac	376
Ile Ile Leu Met Lys	
	20
tgtctcaagaa raaatggccc ttttagaasc tgtgatggac tgtggctttg gaaattggca	436
ggatgtagcc aatcaaatgt gcaccaarac caaggaggag tgtgagaagc actatatgaa	496
gcatttctac aataaccctc tgtttgcac trscctgctg aacctgaaac aascagrnga	556
agcaaaaact gctgacacag ccattccatt tcaactctaca ratgaccctc cccgacckac	616
ctttgactcc ttgctttctc gggacatggc cgggtacwtg ccmgctcgag cagatttcat	676
tgaggaattt gacaattatg cagaatggga cttgagagac attgattttg ttgaagatga	736
ctcggacatt ttacatgctc tgaagatggc tgtggtagat atctatcatt ccaggttaaa	796
ggagagacaa agacgaaaaa aaaaaaa	823

<210> 316

<211> 823
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 191..553

<221> sig_peptide
 <222> 191..304
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LAFLSCLAFLVLD/TQ

<221> polyA_signal
 <222> 766..771

<221> polyA_site
 <222> 804..817

<400> 316
 aactctgcag ggccctccaag gccaggttc agggctggga ctcagtcctg aggcactggg 60
 gagccatgag gggctgtggc agggaggggc aggggtgtgga aagactcccc tggggccatg 120
 gtggagatgt gctgaggtct tctccctgat cgtcttctcc tccctgctga ccgacggcta 180
 ccagaackag atg gag tct ccg cag ctc cac tgc att ctc aac agc aac 229
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
 -35 -30
 agc gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc ctc 277
 Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
 -25 -20 -15 -10
 agc tgc ctg gcc ttc ctc gtc ctg gac aca cag gag acc cgc att gcc 325
 Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
 -5 1 5
 ggc acc cgc ttc aag aca gcc ttc cag ctc ctg gac ttc atc ctg gct 373
 Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala
 10 15 20
 gtt ctc tgg gca gtt gtc tgg ttc atg ggt ttc tgc ttc ctg gcc aac 421
 Val Leu Trp Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn
 25 30 35
 caa tgg cag cat tcg ccg ccc aaa gar kkc ctc ctg ggg agc agc agt 469
 Gln Trp Gln His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser
 40 45 50 55
 gcc cag gca gcc atc ggc stt cac ctt ctt ctc cat cct tgt ctg gat 517
 Ala Gln Ala Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp
 60 65 70
 att cca rgc cta cct ggc akk cca gga cct ccg aaa tgatgctcca 563
 Ile Pro Xaa Leu Pro Gly Xaa Pro Gly Pro Pro Lys
 75 80
 gtcccttacm arcgcttccct ggatgaaggt ggcagtggts kkaacaccct ccccttgecc 623
 tctgccaaca gcctgtgaac atgcccacca ctggcccaaa cagcctgagt tatgctagct 683
 ctgcccctgtc cccctgtctg accgctcmaa agtccccccg gcttgctatg atgcctgaca 743
 actaaatc cttatccaaa tcaataaaga gagaatcctc cctccagaag ggtttctaaa 803
 aacaaaaaaa aaaahncctt 823

<210> 317
 <211> 1112
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 106..603

<221> sig_peptide

<222> 106..216

<223> Von Heijne matrix

score 4.30000019073486

seq LWEKLTLLSPGIA/VT

<221> polyA_site

<222> 1102..1112

<400> 317

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agcgattgcg aatcctccgc tgaggtgatt tggatatccc tagaacgttg agggcacgag      60
tcgggtcctg agaccaggtc ctcagccagc agagccacgt tcctt atg agc acc gtg      117
                                     Met Ser Thr Val
                                     -35
ggt tta ttt cat ttt cct aca cca ctg acc cga ata tgc ccg gcg cca      165
Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile Cys Pro Ala Pro
          -30                      -25                      -20
tgg gga ctc cgg ctt tgg gag aag ctg acg ttg tta tcc cca gga ata      213
Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu Ser Pro Gly Ile
          -15                      -10                      -5
gct gtc act ccg gtc cag atg gca ggc aag aag gac tac cct gca ctg      261
Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp Tyr Pro Ala Leu
          1                      5                      10                      15
ctt tcc ttg gat gag aat gaa ctc gaa gag cag ttt gtg aaa gga cac      309
Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe Val Lys Gly His
          20                      25                      30
ggt cca ggg ggc cag gca acc aac aaa acc agc aac tgc gtg gtg ctg      357
Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn Cys Val Val Leu
          35                      40                      45
aar mac atc ccc tca ggc atc gtt gta aag tgc cat cag aca aga tca      405
Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His Gln Thr Arg Ser
          50                      55                      60
gtt gat cag aac aga aag cta gct cgg aaa atc cta caa gag aaa gta      453
Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu Gln Glu Lys Val
          65                      70                      75
rat gtt ttc tac aat ggt gaa aac agt cct gtt cac aaa gaa aaa cga      501
Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His Lys Glu Lys Arg
          80                      85                      90                      95
gaa gcg gcg aag aaa aaa car gaa agg aaa aaa aga gca aag gaa acc      549
Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg Ala Lys Glu Thr
          100                      105                      110
ctg gaa aaa aag aas ctm ctt aaa raa ctg tgg gag tca agt aaa aag      597
Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu Ser Ser Lys Lys
          115                      120                      125
gtc cac tgagaaaaga attagagatt ccaactgaca gaatctgcca gaagctccca      653
Val His
gggaataatg gtggcgagtt ccatcaccag cattattata gtgcttcaaa agaaatatatt      713
ttgatgaact taaaagacaa caaatattatt taaatggtgc actaaactgt agtgaacaga      773
gacatgcacg attcaagaat aaaactcggc cgggcacggg ggacggtgcc tcacatctgt      833
aatcccagca ctttgggagg ccgaggcggg cggatcactt gaggtcagga gtttgagacc      893
agcctggcca acatggtgaa acccgtctc tactaaaaat acaaaaaatt agccaggcat      953
ggtggcgggc acctgtaatc ccagctactc gggaggccga ggcaggagaa ttgcgtgaac      1013
ctgggaggcg gaggttgtag tgagctgaga tcgcgccact gcactcaagc ctgggcaaca      1073
cctgggtgac agagcaagac cccatcycaa aaaaaaaaaa      1112

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<210> 318

<211> 1623

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..586

<221> sig_peptide
<222> 47..124
<223> Von Heijne matrix
score 6.30000019073486
seq GVGLVTLLGLAVG/SY

<221> polyA_signal
<222> 1583..1588

<221> polyA_site
<222> 1614..1623

<400> 318
agggatctgt cggcttgtca ggtggtggag gaaaaggcgc tccgtc atg ggg atc 55
Met Gly Ile
-25
cag acg agc ccc gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act 103
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr
-20 -15 -10
ctg ctc ggc ctg gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg 151
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg
-5 1 5
cct cag gtc act ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg 199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu
10 15 20 25
cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc 247
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala
30 35 40
ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc 295
Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile
45 50 55
tac ctc tcc acm mga att gat ggc agc ctg gtc atc agg cca tac act 343
Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr
60 65 70
cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc mtc aag 391
Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Xaa Lys
75 80 85
gtc tac ctg aag ggt gtg cac ccc aaa ttt cct gag gga ggg aar atg 439
Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met
90 95 100 105
tct cak tac ctg gat asc ctg aaa gtt ggg gat btg gtg gaa ttt csg 487
Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val Glu Phe Xaa
110 115 120
ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att 535
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile
125 130 135
cag ccc aac aag aat ctc cac cag aac ccc gag tgg cga aga aac tgg 583
Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg Arg Asn Trp
140 145 150
gaa tgattgccgg cgggacagga atcaccccaa tgctacagct gatccgggcc 636
Glu
atcctgaaag tccctgaaga tccaaccag tgctttctgc tttttgccaa ccagacagaa 696
aaggatatca tcttgcgga ggacttagag gaactgcagg cccgctatcc caatcgcttt 756
aagctctggt tcaactctgga tcatcccca aaagrttggg cctacagcaa gggcttctgtg 816
actgccgacw tgatccggga acacctgccc gctccagggg atgatgtgct ggtactgctt 876

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tgtggggccmc ccccaatggt gcagctggcc tgccatccca acttggaaca actgggctac 936
tcacaaaaga tgcgattcac ctactgagca tcctccagct tccctggtgc tggtcgctgc 996
agttgttccc catcagtact caagcactak aagccttagr ktcctktcct cagagtttca 1056
ggtttttttca gttrsatcha gagctgaaat ctggatagta cctgcaggaa caatattcct 1116
gtagccatgg aagagggcca aggcctcagtc actccttgga tggcctccta aatctccccg 1176
tggcaacagg tccaggagag gcccatggag cagtctcttc catggagtaa gaaggaaggg 1236
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acctatgagc aaatctgtat gtgtgagtat aagttgagca tagcatactt ccagaggtgg 1416
tcttatggag atggcaagaa aggaggaaat gatttcttca gatctcaaag gagtctgaaa 1476
tatcatattt ctgtgtgtgt cdctctcagc ccctgcccad gctagaggga wacagctact 1536
gataatcgaa aactgctgtt tgtgggcarg aaccctggc tgtgcaaata atggggctga 1596
ngccctgtgt gatattgaaa aaaaaaa 1623

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<210> 319

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 99..371

<221> sig_peptide

<222> 99..290

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<223> Von Heijne matrix
      score 3.79999995231628
      seq LFIVVCVICVTLN/FP

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<221> polyA_signal

<222> 491..496

<221> polyA_site

<222> 513..524

<400> 319

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attggattag tagaattgct tttgtcattc cattgttttc atatatttgt ttgggacatt 60
ttactttttt ctgttaacgc ttaccctagr aattagaa atg aca cca cgt att ctt 116
                               Met Thr Pro Arg Ile Leu
                               -60
agc gaa gtc cag ttt tca gca ttt tgt cct tat tgg aca ata gca agg 164
Ser Glu Val Gln Phe Ser Ala Phe Cys Pro Tyr Trp Thr Ile Ala Arg
      -55                               -50                               -45
ata tta gaa cgt gtt ggt tcc gcg tgc ttc cgt ctt gag tta tgt gct 212
Ile Leu Glu Arg Val Gly Ser Ala Cys Phe Arg Leu Glu Leu Cys Ala
      -40                               -35                               -30
gct att gtc gga tat ttt gtc tta gat gta cgt act ttc ctg ttc att 260
Ala Ile Val Gly Tyr Phe Val Leu Asp Val Arg Thr Phe Leu Phe Ile
      -25                               -20                               -15
gtg gta tgt gta att tgc gtt act ttg aat ttt cca cgt ttt tac ttt 308
Val Val Cys Val Ile Cys Val Thr Leu Asn Phe Pro Arg Phe Tyr Phe
      -10                               -5                               1                               5
ctt tgt ctc tca tca ctt acc gct ttt ggg acc ccc ccc atc ggg gtt 356
Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly Thr Pro Pro Ile Gly Val
      10                               15                               20
cac att ccc tct ccc tararcacac tccttggat ttctcradt ggggtctgct 411
His Ile Pro Ser Pro
      25
gcggtgaagc tttcccatth tatgtgcaga ttattttcag agggatatata gaattcaggg 471
agctgtttcg ttgtagcaca ttaaaaaatat tttcccactt caaaaaaaaa aaacc 526

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<210> 320
 <211> 989
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..814

<221> sig_peptide
 <222> 44..112
 <223> Von Heijne matrix
 score 8.30000019073486
 seq VRLLLXLLLLLLIA/LE

<221> polyA_site
 <222> 978..989

<400> 320
 aaatgtgtac acgcccagct tcctgcctgt tactctccac agt atg cga aga ata 55
 Met Arg Arg Ile
 -20
 tcc ctg act tct agc cct gtg cgc ctt ctt ttg tdt ctg ctg ttg cta 103
 Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Leu Leu Leu
 -15 -10 -5
 cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac 151
 Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
 1 5 10
 ttc act ata aaa tca ttg tcc aga cct gga cag ccc tgg tgt gaa gcg 199
 Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala
 15 20 25
 cat gtc ttc ttg aat aaa aat ctt ttc ctt cag tac aac agt gac aac 247
 His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn
 30 35 40 45
 aac atg gtc aaa cct ctg ggc ctc ctg ggg aag aag gta tat gcc acc 295
 Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr
 50 55 60
 agc act tgg gga gaa ttg acc caa acg ctg gga gaa gtg ggg cga gac 343
 Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp
 65 70 75
 ctc agg atg ctc ctt tgt gac atc aaa ccc car ata aag acc agt gat 391
 Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile Lys Thr Ser Asp
 80 85 90
 cct tcc act ctg caa gtc kar atk ttt tgt caa cgt gaa gca gaa cgg 439
 Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg Glu Ala Glu Arg
 95 100 105
 tgc act ggt gca tcc tgg cag ttc gcc acc aat gga gag aaa tcc ctc 487
 Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly Glu Lys Ser Leu
 110 115 120 125
 ctc ttt gac gca atg aac atg acc tgg aca gta att aat cat gaa gcc 535
 Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile Asn His Glu Ala
 130 135 140
 agt wag atc aag gag aca tgg aag aaa gac aga ngg ctg gaa aak tat 583
 Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa Leu Glu Xaa Tyr
 145 150 155
 ttc agg aag ctc tca aar gga gac tgc gat cac tgg ctc agg gaa ttc 631
 Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp Leu Arg Glu Phe
 160 165 170
 tta ggg cac tgg gaa gca atg cca raa ccg ama gtg tcm cca rta aat 679


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Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val Ser Pro Xaa Asn
  175                      180                      185
gct tca raw atc cac tgg tct tct tct art cta cca raw ara tgg atc      727
Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro Xaa Xaa Trp Ile
  190                      195                      200                      205
atc ctg ggg gca ttc atc ctg tta vtt tta atg gga att gtt ctc atc      775
Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly Ile Val Leu Ile
                      210                      215                      220
tgt gtc tgg tgg caa aat ggc ara ara tcc acc tad arg tgataccacg      824
Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa Xaa
                      225                      230
gcggcgcaaaa attgttcacc tgtggtcctc gatcgctgac agccttggct cccactgctg      884
tgtgttcctt gagtcaagtg gaggcggagc ctgcaatgag cggaratcgc gcctctgcat      944
tccagtcttg gcaacagarc aagactccgt ctcaaaaaaa aaaaa      989

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<210> 321

<211> 1017

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 3..581

<221> sig_peptide

<222> 3..182

<223> Von Heijne matrix

score 6.69999980926514

seq LWPFLTWINPALS/IC

<221> polyA_site

<222> 1006..1016

<400> 321

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ac atg tgc cct agt ctg gaa gag gct ccc agt gtc aag ggg act ctg      47
  Met Cys Pro Ser Leu Glu Ala Pro Ser Val Lys Gly Thr Leu
  -60                      -55                      -50
ccc tgc tca gga caa cag cag cct ttc ccg ttt gga gcc tca aac atc      95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile
-45                      -40                      -35                      -30
cca cta ctc ctg ggc agg agc aga aag gtg gct cga ggt gca ccg gtc      143
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val
                      -25                      -20                      -15
ctg tgg cca ttt ctc act tgg ata aac cct gca ctg tcc atc tgt gac      191
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp
                      -10                      -5                      1
ccc tta gga tcc tgc gga tgg cyw tgc cac acg gcc car gtc cct gcg      239
Pro Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala
  5                      10                      15
ccc ctg car ttg cct act gcc tgt cct ccc ctc cca cat ggc acc cgg      287
Pro Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg
  20                      25                      30                      35
gct gta ggc ccc acg cca ggc ctc ctc cct gag gct gca gcc cca sgc      335
Ala Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa
                      40                      45                      50
acg tgk ggg gca ctg tcc tca cgc agc agg cac tgg tca tgt tcc att      383
Thr Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile
                      55                      60                      65
gtc arc tgc ctc cac ctg cac ara ctc ctg tct gtg gag acc aga arc      431
Val Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa

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      70              75              80
ttc cas aaa cat ctg ttg gtg ctg ctg gtg gct gtg gcc cat agt gtt 479
Phe Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val
      85              90              95
ctg gaa cca cct gcc ctg gtc cca aat gtg cag tgt gag atg tgc aca 527
Leu Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr
      100             105             110             115
cac tca ggg ccc cgt gac ctg gaa gcc gca gtc gtg tcc cca gca cct 575
His Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro
              120              125              130
tgg gaa tgagcctgtc ctctgtgtga aggaggggggt gggttctcaaa ccactgactc 631
Trp Glu
ttggtgtctca ggaggggcct gctgctgtcc tgggcatggg gtggtcattg ttcaagactg 691
aggcagactc agtctttgaa aggggtgcaga ggccaggcgc ggtggctcac gcctgtaatt 751
ccagcacttt gggaggccaa ggtggacaga tcatgaggtc aggagttcga gaccagcctg 811
gccaatacgg tgaaaccgca tctctactaa rraatawcaaw aaattagtcg ggcattgggtg 871
atgtgtgctt gtagtcccag ctactcatga ggyctgaggc agaagaatca cctgaatctg 931
ggaggcagag gttgcagtga accaagatcg cacgactgta caccagcctg ggcgacagag 991
tgagactccg tctcaaaaaa aaaaam 1017

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<210> 322

<211> 529

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 107..427

<221> sig_peptide

<222> 107..190

<223> Von Heijne matrix

score 3.79999995231628

seq RFLSLSAADGSDG/SH

<221> polyA_signal

<222> 499..504

<221> polyA_site

<222> 516..529

<400> 322

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aaagtcagcg ctggagtcgg ctaggcggct ggaaacggcg gctgccgccg gtgactcagg 60
gaggcgggag gccgmsggmg gagctcttcc tgcaggcgtg garacc atg gtg ctc 115
                               Met Val Leu
acg ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt 163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25              -20              -15              -10
ctg tcc gca gcc gac ggc agc gat ggc agc cac gac agc tgg gac gtg 211
Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser Trp Asp Val
              -5              1              5
gag cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt 259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
      10             15             20
tcc cac acc gac gtt acc aag aag gat ctg aag gtg tgt gtg gaa ttt 307
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys Val Glu Phe
      25             30             35
gak ggg gaa tct tgg agg aaa aga aga tgg ata gaa gtc tac agc ctt 355
Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val Tyr Ser Leu
      40             45             50             55

```

```

cta agg aaa gca ttt tta gta aaa cat aat ttg gtt tta gct gaa cga      403
Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu Ala Glu Arg
      60                      65                      70
aag tca cct gaa att tct tgg ggt taaccatctt tagttaaatg gaattttaat      457
Lys Ser Pro Glu Ile Ser Trp Gly
      75
ttaaatgacg ctttgctaatt ttttaagtgtt aagcattttg cattaaaata ttcataata      517
aaaaaaaaaa aa                                                         529

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```

<210> 323
<211> 1046
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 45..407

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<221> sig_peptide
<222> 45..83
<223> Von Heijne matrix
      score 5.69999980926514
      seq MLVLRSA LTRALA/SR

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<221> polyA_signal
<222> 1008..1013

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```

<221> polyA_site
<222> 1032..1042

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<400> 323
aaaaggacac ggctggctgc ttttctcagc gccgaagccg cgcc atg ctc gtc ctc      56
                                         Met Leu Val Leu
                                         -10
aga agc gcc ctg act cgg gcg ctg gcc tca cgg acg ctg gcg cct cag      104
Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr Leu Ala Pro Gln
      -5                      1                      5
atg tgc tca tct ttt gct acg gga ccc aga caa tac gat gga ata ttc      152
Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Ile Phe
      10                      15                      20
tat gaa ttt cgt tct tat tac ctt aag ccc tca aag atg aat gag ttc      200
Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys Met Asn Glu Phe
      25                      30                      35
ctg gaa aat ttt gag aaa aac gct caa ctt cgg aca gct cac tct gaa      248
Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr Ala His Ser Glu
      40                      45                      50                      55
ttg gtt gga tac tgg agt gta kaa ttt gga ggc aga atg awt aca gtg      296
Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg Met Xaa Thr Val
      60                      65                      70
ttt cat att tgg aag tat gat aat ttt gct cat cga act gaa ttt cag      344
Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Glu Phe Gln
      75                      80                      85
aaa gcc ttg gcc aaa gat aag gaa tgg caa gaa caa ttc ctc att cca      392
Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Pro
      90                      95                      100
aat ttg gct ctc aat tgataaacia gatagtgaga ttracttatct ggtaccatgg      447
Asn Leu Ala Leu Asn
      105
tgcaaattag aaaaacctcc aaaagaagga gtctatgaac tggccacttt tcagatgaaa      507
cctggtgggc cagctctgtg gggatgatgca tttaaaaggg cagttcatgc tcatgtcaat      567

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ctaggctaca caaaactagt tggagtgttc cacacagagt acggagcact caacagagtt 627
catgttcttt ggtggaatga gagtgcagat agtcgtgcag ctgggagaca taagtcccat 687
gaggatccca gagtgtgtgc agctgttcgg gaaagtgtca actacctagt atctcagcag 747
aatatgcttc tgattcctac atcgttttca ccactgaaat agttttctac tgaaatacaa 807
aacatttcat taactgctat aggatctgtc tgctaattgt gcttaaattc tcccaagagg 867
ttctcacttt tatttgaagg aggtggttaag ttaatttgct atgtttcttg cattatgaag 927
gctacatctg tgctttgtaa gtaccacttc aaaaaatakt tctgtttact ttctgcatgg 987
tatttcagtg tctgtcatatc attaaaaata cttgtcactg tttyaaaaaa aaaaammcc 1046

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<210> 324

<211> 880

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 201..332

<221> sig_peptide

<222> 201..251

<223> Von Heijne matrix

score 7.80000019073486

seq VLWLISFFFTDGHG

<221> polyA_site

<222> 869..880

<400> 324

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aattgctgat ggatcagtga gcctgtgttc atgccagtga gctgctgtgg ctcagatact 60
gatactttct ttccaaacag cataagaagt gattgancca caagtatact gaaggmargg 120
yhccowsvar tyctggwgtg amgagataaa tcaccagtca cagactatgc acccgactgc 180
tgctgttcag tccagggaaa atg aaa gtt gga ctg tgg ctc att tct ttc 233
                Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe
                -15                               -10
ttc acc ttc act gac ggc cac ggt ggc ttc ctg ggg gtg agt tgg tgc 281
Phe Thr Phe Thr Asp Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys
    -5              1              5              10
tat gtc tca tat ctc ttc tca act aac tct cct ctc tgc ttc cgg cgc 329
Tyr Val Ser Tyr Leu Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg
                15              20              25
att tagaaccct cactctctag gggactgcaa ctgcataatt taatgtactt 382
Ile
gagatcagaa gtctgtgagt ctcgtttcaa cattaccaac attcactgtg tggccttgga 442
taagtragtc atttcatctc ttcggagctt agatgatcma actgcaarag gaggatcttt 502
gattamacta tcttagagat cttttccagt tcaacacatg ctgtactatg gcttctcgga 562
tgcagaaaaa tcacatggat ggacattagc aatccttara cactgtcttt cctgtctaca 622
ctcgcttgag tgatgckttc atctaggatc atgggtttta tattctctac atgctgatga 682
ctcccagctg tatagctcca tctcagaacc tctccctgtt ccacactcac atatccatta 742
cctacgtgtt atttccagct gggaaatcca gcggaacctc ggnaacttca tttgnttcaa 802
aatcgnaacc caatccttct tgcctatctc agcaagtggg atcactatct ttccagctac 862
ttaggcaaaa aaaaaaaaaa 880

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<210> 325

<211> 1217

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 217..543

<221> sig_peptide

<222> 217..255

<223> Von Heijne matrix

score 6.40000009536743

seq MCLLTALVTQVIS/LR

<221> polyA_site

<222> 1206..1217

<400> 325

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aatgccagtgc tcagcttctc tccgaaaact gggtaatacgc aaatgggtctt tattgggtgtg      60
gaacactcga gctgagaaac atttttaggat ctttgtgtct tttgtgatga tttgtttct      120
graagrwgga aasctgtcta aaaatattca agtgtgcaac caaggattta gatgaagcca      180
gcaaacaaag gaatcatgta atcaggacct gagcga atg tgc tta ctc acg gcg      234
                                Met Cys Leu Leu Thr Ala
                                -10
tta gtt aca cag gtg att tcc tta aga aaa aat gca gag aga act tgt      282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
-5                                1                                5
tta tgc aag agg aga tgg ccc tgg ngc ccc tgc ccc cgg atc tac tgc      330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
10                                15                                20                                25
tca tcc acc cca tgc gat tcc aaa ttc ccc acc gtc tac tcc agt gcc      378
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser Ala
30                                35                                40
cca ttc cat gcc ccc ctc ccc gtc cag aat tcc tta tgg ggg cac ccg      426
Pro Phe His Ala Pro Leu Pro Val Gln Asn Ser Leu Trp Gly His Pro
45                                50                                55
ctc cat ggt tgt tcc tgg caa tgc cac cat ccc cag gga car aat ctc      474
Leu His Gly Cys Ser Trp Gln Cys His His Pro Gln Gly Gln Asn Leu
60                                65                                70
cag cct gcc agt ctc cad acc cat ctc tcc aag ccc aag cgc cat ttt      522
Gln Pro Ala Ser Leu Xaa Thr His Leu Ser Lys Pro Lys Arg His Phe
75                                80                                85
ara aar aar rra tgt caa gcc tgcataaac atgagtggca aaaacattgc      573
Xaa Lys Lys Xaa Cys Gln Ala
90                                95
aatgtacara aatgagggtt tctatgctga tccttacctt tatcacgagg gacggatgag      633
catascctca tcccatggtg gacacccact ggatgtcccc gaccacatca ttgcatatca      693
ccgcaccgcc atccggtcag cgagtgtcta ttgtaacccc tcaatgcaag cggaaatgca      753
tatggaacaa tcaactgtaca gacagaaatc aaggaaatat ccggatagcc atttgcctac      813
actgggctcc aaaacacccc ctgcctctcc tcacagaktc agtgacctga ggatgataga      873
catgcacgct cactataatg cccacggccc cctcacacc atgcagccag accgggcctc      933
tccgagccgc caggccttta aaaaggagcc aggcaccttg gtgtatatag aaaagccacg      993
gagcgctgca ggattatcca gccttgtaga cctcgccctt cctctaattg agaagcaagt     1053
ttttgcctac agcacggcga caatacccaa agacagagag accagagaga ggatgcaagc     1113
catggagaaa cagattgccg gtttaactgg ccttgctcag tctgcgcttt ttaaagggcc     1173
cattacaagt tatagcaaar atgcgtctag ctaaaaaaaa aaaa                        1217

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<210> 326

<211> 959

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..446

<221> sig_peptide
 <222> 18..140
 <223> Von Heijne matrix
 score 4.09999990463257
 seq GILILWIIRLLFS/KT

<221> polyA_signal
 <222> 930..935

<221> polyA_site
 <222> 948..959

<400> 326
 aaaggaagcgc gctaact atg gcg acc gcc acg gag cag tgg gtt ctg gtg 50
 Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val
 -40 -35
 gag atg gta cag gcg ctt tac gag gct cct gct tac cat ctt att ttg 98
 Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu
 -30 -25 -20 -15
 gaa ggg att ctg atc ctc tgg ata atc aga ctt ctt ttc tct aag act 146
 Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr
 -10 -5 1
 tac aaa tta caa gaa cga tct gat ctt aca gtc aag gaa aaa gaa gaa 194
 Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu
 5 10 15
 ctg att gaa gag tgg caa cca gaa cct ctt gtt cct cct gtc cca aaa 242
 Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys
 20 25 30
 gac cat cct gct ctc aac tac aac atc gtt tca ggc cct cca agc cac 290
 Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His
 35 40 45 50
 aaa act gtg gtg aat gga aaa gaa tgt ata aac ttc gcc tca ttt aat 338
 Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn
 55 60 65
 ttt ctt gga ttg ttg gat aac cct agg gtt aag gca gca gct tta gca 386
 Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala
 70 75 80
 tct cta aag aag tat ggc gtg ggg act tgt gga ccc tgt gga ttt tat 434
 Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr
 85 90 95
 ggc aca ttt gaa tgaaratgaa ggatcattga tttccttgtg tatggataat 486
 Gly Thr Phe Glu
 100
 ccgggaacag gccaaactaaa tatttgatga atgtatgatt tcaaatacag tgaattccct 546
 gggagtcacg aaaraagacg gcattttatg gttgttttta ttaagtgtat attcctttgct 606
 cctgaaaatg ttattaaata attgtttagg ccgggcatgg tggctcatgc ctgtaatccc 666
 agcactttca aaggctgagg caggcagatc acctgaggtc aggagttcaa aaccagcctg 726
 gccaacatgc tgaaacctcg tctctactaa aaatacaaaa attagctggg cgtgggtggg 786
 grtgctgtg gtcccagctr cgtgggaggc tgaggtggga gaattgcttc aacctgggag 846
 gcggagggtg cagtgagccg agatcatgcc actgcactcc agcctgggca acagagcaag 906
 actgtctcaa aaataaataa ataaataaaa ttgtttaaat gaaaaaaaaa aaa 959

<210> 327
 <211> 921
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 29..724

<221> sig_peptide

<222> 29..118

<223> Von Heijne matrix

score 3.90000009536743

seq VAHALSLPAESYG/NX

<221> polyA_signal

<222> 886..891

<221> polyA_site

<222> 910..920

<400> 327

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aaggagccac gctttcggggg gttgcaag atg gcg gcc acc agt gga act gat      52
                               Met Ala Ala Thr Ser Gly Thr Asp
                               -30                               -25

gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg ctt tct ctc      100
Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala Leu Ser Leu
      -20                               -15                               -10

cca gca gag tcg tat ggy aac grt yct gac att gag atg gct tgg gcc      148
Pro Ala Glu Ser Tyr Gly Asn Xaa Xaa Asp Ile Glu Met Ala Trp Ala
      -5                               1                               5                               10

atg aga gca atg cag cat gct gaa gtc tat tac aag ctg att tca tca      196
Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu Ile Ser Ser
      15                               20                               25

gtt gac cca cag ttc ctg aaa ctc acc aaa gta gat gac caa att tac      244
Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp Gln Ile Tyr
      30                               35                               40

tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat gtg ttg grc      292
Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp Val Leu Xaa
      45                               50                               55

cca gaa gan ctc aag tca gaa tca gcn aaa gag ccc cca gga tac aat      340
Pro Glu Xaa Leu Lys Ser Glu Ser Ala Lys Glu Pro Pro Gly Tyr Asn
      60                               65                               70

tct ttg cca ttg aaa ttg ctc gga acc ggg aag gct ata aca aag ctg      388
Ser Leu Pro Leu Lys Leu Leu Gly Thr Gly Lys Ala Ile Thr Lys Leu
      75                               80                               85                               90

ttt ata tca gtg ttc agg aca aag aag gag aga aag gag tca aca atg      436
Phe Ile Ser Val Phe Arg Thr Lys Lys Glu Arg Lys Glu Ser Thr Met
      95                               100                               105

gag gag aaa aaa gag ctg aca gtg gag aag aag aga aca cca aga atg      484
Glu Glu Lys Lys Glu Leu Thr Val Glu Lys Lys Arg Thr Pro Arg Met
      110                               115                               120

gag gag aga aag gag ctg ata gtg gag aag aaa aag agg aag gaa tca      532
Glu Glu Arg Lys Glu Leu Ile Val Glu Lys Lys Lys Arg Lys Glu Ser
      125                               130                               135

aca gag aag aca aaa ctg aca aag gag gag aaa aag gga aag aag ctg      580
Thr Glu Lys Thr Lys Leu Thr Lys Glu Glu Lys Lys Gly Lys Lys Leu
      140                               145                               150

aca aag aaa tca aca aaa gtg gtg aaa aag cta tgt aag gta tac agg      628
Thr Lys Lys Ser Thr Lys Val Val Lys Lys Leu Cys Lys Val Tyr Arg
      155                               160                               165                               170

gaa cag cac tct aga agc tat gac tca att gag act aca agt acc acg      676
Glu Gln His Ser Arg Ser Tyr Asp Ser Ile Glu Thr Thr Ser Thr Thr
      175                               180                               185

gtg cta ctt gca cag acc cct ttg gtt aaa tgt aaa ttc ttg tac aat      724
Val Leu Leu Ala Gln Thr Pro Leu Val Lys Cys Lys Phe Leu Tyr Asn
      190                               195                               200

tgaaggatac gcagaaggac atctttctag tctaacagtc aggagctgct ctgggtcattc      784
ccttgatga actggtctaa agactgttag tggggtgtta gttgattttt cctggtatac      844

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tgttttcttggt ctgacactac tgggtcaagta agaaatttgt aaataaattt cttttgggttc 904
 ttattaamaa aaaaaas 921

<210> 328
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 404..586

<221> sig_peptide
 <222> 404..466
 <223> Von Heijne matrix
 score 4.09999990463257
 seq SLMFFSMMATCTS/NV

<221> polyA_signal
 <222> 1304..1309

<221> polyA_site
 <222> 1334..1344

<400> 328
 ataatttaat gcaaaatata cttttatgaa ttcatgtta atattgtgaa atattaaaat 60
 aattccacaa tagttgagaa aaatgagcat ttttttccat ttttaaaaaa tgcataagaaa 120
 agacaatttt aaaatcctgg gamccawatt tatttagaag tagctgttag taaaacatta 180
 gaaaaggagt caggccatba ggttatttat nbnaatctct aagcaattag gntgaagtta 240
 ttaagtcaag cctagaaaag ctgcctcctt gtaaggcttt catgacaatg tatagtaatc 300
 brcagtgtcc aattcttcgc actcctcagg aatatcacta cctcaggtta cggtaacacag 360
 gctataattg atgatgatgt tcagataact gaagacacaa taa atg aca ttc aga 415
 Met Thr Phe Arg
 -20
 cat cag gac aat tcc ctc atg ttc ttt tct atg atg gcc acc tgt acc 463
 His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met Ala Thr Cys Thr
 -15 -10 -5
 agc aac gtg ggt ttc acc cac aca acg atg aac tgt tct ctt act tct 511
 Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys Ser Leu Thr Ser
 1 5 10 15
 cca gtt gat ttt aaa gac ttg tta aga gtc tta cta ata aaa ttt ggg 559
 Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu Ile Lys Phe Gly
 20 25 30
 tat gat aga aaa tcc aca atc aaa tct tgaaccaa aacatattaa 606
 Tyr Asp Arg Lys Ser Thr Ile Lys Ser
 35 40
 attactaata tttaagtgat ggaagacaca caaaaaactt aaaagcacga acaacctaac 666
 ttgaaaaara attttaaaat atgattaacc tgaaraaaar araatcctaa ragccaaagc 726
 tcctttttat ttagcttgga attttcctat tgggttcctaa caaactgtcc caatgtcata 786
 taaggaaaca tgatctatta cattccttta taacaacgtg gararactat aaacctatgt 846
 aagtagtaaa actatatcag adactcagga ractgactww aaggcctgga tctgcagtgt 906
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